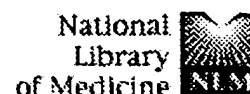


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L13	L12 AND receptor	114	L13
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L10	(530/351,387.1.CCLS.)	0	L10
L9	L8 AND MCP-1	17	L9
L8	((435/326 )!.CCLS. )	533	L8
L7	L6 AND MCP-1	38	L7
L6	((424/130.1 )!.CCLS. )	1180	L6
L5	Couglin-Shaun.IN.	0	L5
L4	Couglin.IN.	0	L4
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

















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


















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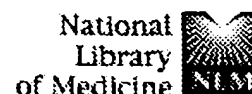
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

















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












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
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
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
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











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=> S MCP-1  
22 FILES SEARCHED...  
42 FILES SEARCHED...  
L1 31673 MCP-1

=> S L1 AND antibody  
27 FILES SEARCHED...  
62 FILES SEARCHED...  
L2 6620 L1 AND ANTIBODY

=> DUP REM L2  
DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,  
DRUGLAUNCH, DRUGMONOG2, DRUGUPDATES, FEDRIP, FOREGE, GENBANK, KOSMET,  
MEDICONF, NUTRACEUT, PCTGEN, PHAR, PHARMAML, RDISCLOSURE, SYNTHLINE'.  
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PROCESSING IS APPROXIMATELY 14% COMPLETE FOR L2  
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PROCESSING IS APPROXIMATELY 97% COMPLETE FOR L2

L3 3017 DUP REM L2 (3603 DUPLICATES REMOVED)

=> S L3 AND receptor  
19 FILES SEARCHED...  
34 FILES SEARCHED...  
57 FILES SEARCHED...  
60 FILES SEARCHED...  
L4 2059 L3 AND RECEPTOR

=> S L4 AND PY<=1995  
'1995' NOT A VALID FIELD CODE  
6 FILES SEARCHED...  
9 FILES SEARCHED...  
13 FILES SEARCHED...  
17 FILES SEARCHED...  
'1995' NOT A VALID FIELD CODE  
30 FILES SEARCHED...  
'1995' NOT A VALID FIELD CODE  
'1995' NOT A VALID FIELD CODE  
42 FILES SEARCHED...  
'1995' NOT A VALID FIELD CODE  
48 FILES SEARCHED...  
49 FILES SEARCHED...  
'1995' NOT A VALID FIELD CODE  
55 FILES SEARCHED...  
59 FILES SEARCHED...  
L5 38 L4 AND PY<=1995

=> D L5 1-38

L5 ANSWER 1 OF 38 ADISNEWS COPYRIGHT (C) 2003 Adis Data Information BV on  
STN  
ACCESSION NUMBER: 1995:194 ED: 8 Aug 2001 UP: 8 Aug 2001  
DOCUMENT NUMBER: 11738324-800314413  
TITLE: Symposia: News from Digestive Disease Week.  
SOURCE: INPHARMA \*\*\*12 Jun 1995\*\*\* ISSN: 1173-8324  
DOCUMENT TYPE: (MIX)  
WORD COUNT: 1744

L5 ANSWER 2 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1996:77078 BIOSIS  
DN PREV199698649213  
TI Characterization of transendothelial chemotaxis of T lymphocytes.  
AU Roth, Stephen J.; Carr, Michelle Woldemar; Rose, Shayla S.; Springer,  
Timothy A. [Reprint author]  
CS Center Blood Research, 200 Longwood Ave., Boston, MA 02115, USA  
SO Journal of Immunological Methods, (1995) Vol. 188, No. 1, pp. 97-116.  
CODEN: JIMMBG. ISSN: 0022-1759.  
DT Article  
LA English  
ED Entered STN: 27 Feb 1996  
Last Updated on STN: 27 Feb 1996

L5 ANSWER 3 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1996:21719 BIOSIS  
DN PREV199698593854  
TI High level monocyte chemoattractant protein-1 expression in transgenic  
mice increases their susceptibility to intracellular pathogens.  
AU Rutledge, Barbara J.; Rayburn, Helen; Rosenberg, Robert; North, Robert J.;  
Gladue, Ronald P.; Corless, Christopher L.; Rollins, Barrett J. [Reprint  
author]  
CS Dana-Farber Cancer Inst., 44 Binney St., Boston, MA 02115, USA  
SO Journal of Immunology, (1995) Vol. 155, No. 10, pp. 4838-4843.  
CODEN: JOIMA3. ISSN: 0022-1767.  
DT Article  
LA English  
ED Entered STN: 12 Jan 1996  
Last Updated on STN: 12 Jan 1996

L5 ANSWER 4 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1995:482872 BIOSIS  
DN PREV199598497172  
TI Production of chemokines, interleukin-8 and monocyte chemoattractant  
protein-1, during monocyte: Endothelial cell interactions.  
AU Lukacs, Nicholas W. [Reprint author]; Strieter, Robert M.; Elner, Victor;

CS Univ. Mich. Med. Sch., Dep. Patholol., 1301 Catherine, Ann Arbor, MI  
48109-0602, USA  
SO Blood, (1995) Vol. 86, No. 7, pp. 2767-2773.  
CODEN: BLOOAW. ISSN: 0006-4971.  
DT Article  
LA English  
ED Entered STN: 9 Nov 1995  
Last Updated on STN: 9 Nov 1995

L5 ANSWER 5 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1995:450273 BIOSIS  
DN PREV199598464573  
TI Thrombin regulates expression of monocyte chemoattractant protein-1 in  
vascular smooth muscle cells.  
AU Wenzel, Ulrich O.; Fouqueray, Bruno; Grandaliano, Giuseppe; Kim, Yong-Soo;  
Karamitsos, Costantinos; Valente, Anthony J.; Abboud, Hanna E. [Reprint  
author]  
CS Dep. Med., University Texas Health Sci. Center San Antonio, Floyd Curl  
Dr., San Antonio, TX 78284-7882, USA  
SO Circulation Research, (1995) Vol. 77, No. 3, pp. 503-509.  
CODEN: CIRUAL. ISSN: 0009-7330.  
DT Article  
LA English  
ED Entered STN: 27 Oct 1995  
Last Updated on STN: 27 Oct 1995

L5 ANSWER 6 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1994:395106 BIOSIS  
DN PREV199497408106  
TI Functional and biochemical analysis of the cloned Duffy antigen: Identity  
with the red blood cell chemokine \*\*\*receptor\*\*\*.  
AU Neote, Kuldeep [Reprint author]; Mak, John Y.; Kolakowski., Lee F., Jr.;  
Schall, Thomas J.  
CS Dep. Mol. Genetics and Protein Chemistry, Pfizer Central Res., Eastern Pt  
Rd., Groton, CT 06340, USA  
SO Blood, (1994) Vol. 84, No. 1, pp. 44-52.  
CODEN: BLOOAW. ISSN: 0006-4971.  
DT Article  
LA English  
ED Entered STN: 14 Sep 1994  
Last Updated on STN: 15 Sep 1994

L5 ANSWER 7 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1994:354622 BIOSIS  
DN PREV199497367622  
TI Expression of monocyte chemotactic protein-1 by monocytes and endothelial  
cells exposed to thrombin.  
AU Colotta, Francesco [Reprint author]; Sciacca, Francesca L.; Sironi,  
Marina; Luini, Walter; Rabiet, Marie J.; Mantovani, Alberto  
CS Ist. Ricerche Farmacologiche Mario Negri, Via Eritrea 62, 20157 Milan,  
Italy  
SO American Journal of Pathology, (1994) Vol. 144, No. 5, pp. 975-985.  
CODEN: AJPA44. ISSN: 0002-9440.  
DT Article  
LA English  
ED Entered STN: 23 Aug 1994  
Last Updated on STN: 24 Aug 1994

L5 ANSWER 8 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1994:348040 BIOSIS  
DN PREV199497361040  
TI Identification and characterization of a promiscuous chemokine-binding  
protein in a human erythroleukemic cell line.  
AU Horuk, Richard [Reprint author]; Zi-Xuan, Wang; Peiper, Stephen C.;  
Hesselgesser, Joseph  
CS Dep. Protein Chem., Genentech Inc., 460 Point San Bruno Blvd., South San  
Francisco, CA 94080, USA  
SO Journal of Biological Chemistry, (1994) Vol. 269, No. 26, pp. 17730-17733.  
CODEN: JBCHA3. ISSN: 0021-9258.  
DT Article  
LA English  
ED Entered STN: 8 Aug 1994  
Last Updated on STN: 8 Aug 1994

L5 ANSWER 9 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

DN PREV199497359619  
TI Cytokine expression, upregulation of intercellular adhesion molecule-1,  
and leukocyte infiltration in experimental tubulointerstitial nephritis.  
AU Tang, Winsow W.; Feng, Lili; Mathison, John C.; Wilson, Curtis B. [Reprint  
author]  
CS Dep. Immunol., Scripps Res. Inst., 10666 North Torrey Pines Rd., La Jolla,  
CA 42037, USA  
SO Laboratory Investigation, (1994) Vol. 70, No. 5, pp. 631-638.  
CODEN: LAINAW. ISSN: 0023-6837.  
DT Article  
LA English  
ED Entered STN: 8 Aug 1994  
Last Updated on STN: 8 Aug 1994

L5 ANSWER 10 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1994:181445 BIOSIS  
DN PREV199497194445  
TI Regulation of monocyte chemoattractant protein-1 expression in adult human  
non-neoplastic astrocytes is sensitive to tumor necrosis factor (TNF) or  
\*\*\*antibody\*\*\* to the 55-kDa TNF \*\*\*receptor\*\*\*.  
AU Barna, Barbara P. [Reprint author]; Pettay, James; Barnett, Gene H.; Zhou,  
Ping; Iwasaki, Koichi; Estes, Melinda L.  
CS Dep. Clin. Pathol., L-12, Clevel. Clin. Found., 9500 Euclid Ave.,  
Cleveland, OH 44195-5131, USA  
SO Journal of Neuroimmunology, (1994) Vol. 50, No. 1, pp. 101-107.  
CODEN: JNRIDW. ISSN: 0165-5728.  
DT Article  
LA English  
ED Entered STN: 26 Apr 1994  
Last Updated on STN: 27 Apr 1994

L5 ANSWER 11 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1993:388785 BIOSIS  
DN PREV199396064085  
TI Early and persistent induction of monocyte chemoattractant protein 1 in  
rat cardiac allografts.  
AU Russell, Mary E. [Reprint author]; Adams, David H.; Wyner, Lauri R.;  
Yamashita, Yukari; Halnon, Nancy J.; Karnovsky, Morris J.  
CS Harvard Sch. Public Health, 677 Huntington Avenue, Boston, MA 02115, USA  
SO Proceedings of the National Academy of Sciences of the United States of  
America, (1993) Vol. 90, No. 13, pp. 6086-6090.  
CODEN: PNASA6. ISSN: 0027-8424.  
DT Article  
LA English  
ED Entered STN: 23 Aug 1993  
Last Updated on STN: 23 Aug 1993

L5 ANSWER 12 OF 38 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1992:428524 BIOSIS  
DN PREV199294080649; BA94:80649  
TI RANTES A MONOCYTE AND T LYMPHOCYTE CHEMOTACTIC CYTOKINE RELEASES HISTAMINE  
FROM HUMAN BASOPHILS.  
AU KUNA P [Reprint author]; REDDIGARI S R; SCHALL T J; RUCINSKI D; VIKSMAN M  
Y; KAPLAN A P  
CS DEP MED, SUNY-STONY BROOK, HSC T-16, STONY BROOK, NY 11794-8160, USA  
SO Journal of Immunology, (1992) Vol. 149, No. 2, pp. 636-642.  
CODEN: JOIMA3. ISSN: 0022-1767.  
DT Article  
FS BA  
LA ENGLISH  
ED Entered STN: 22 Sep 1992  
Last Updated on STN: 23 Sep 1992

L5 ANSWER 13 OF 38 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN  
AN 1995:25299199 BIOTECHNO  
TI .alpha. and .beta. chemokines induce NK cell migration and enhance  
NK-mediated cytotoxicity  
AU Taub D.D.; Sayers T.J.; Carter C.R.D.; Ortaldo J.R.  
CS Clinical Services Program, SAIC-Frederick, National Cancer  
Institute-FCRDC, Frederick, MD 21702, United States.  
SO Journal of Immunology, ( \*\*\*1995\*\*\* ), 155/8 (3877-3888)  
CODEN: JOIMA3 ISSN: 0022-1767  
DT Journal; Article  
CY United States  
LA English

L5 ANSWER 14 OF 38 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN  
 AN 1992:22087033 BIOTECHNO  
 TI \*\*\*Receptors\*\*\* for IgG complexes activate synthesis of monocyte  
 chemoattractant peptide 1 and colony-stimulating factor 1  
 AU Hora K.; Satriano J.A.; Santiago A.; Mori T.; Stanley E.R.; Shan Z.;  
 Schlondorff D.  
 CS Department of Medicine, Albert Einstein Coll. of Med., 1300 Morris Park  
 Avenue, Bronx, NY 10461, United States.  
 SO Proceedings of the National Academy of Sciences of the United States of  
 America, ( \*\*\*1992\*\*\* ), 89/5 (1745-1749)  
 CODEN: PNASA6 ISSN: 0027-8424  
 DT Journal; Article  
 CY United States  
 LA English  
 SL English

L5 ANSWER 15 OF 38 CANCERLIT on STN  
 AN 96064693 CANCERLIT  
 DN 96064693 PubMed ID: 7592830  
 TI The promiscuous chemokine binding profile of the Duffy antigen/  
 \*\*\*receptor\*\*\* for chemokines is primarily localized to sequences in the  
 amino-terminal domain.  
 AU Lu Z H; Wang Z X; Horuk R; Hesselgesser J; Lou Y C; Hadley T J; Peiper S C  
 CS Department of Pathology, Henry Vogt Cancer Research Institute, University  
 of Louisville, Kentucky 40292, USA.  
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, \*\*\* (1995 Nov 3) \*\*\* 270 (44) 26239-45.  
 Journal code: 2985121R. ISSN: 0021-9258.  
 CY United States  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS MEDLINE; Priority Journals  
 OS MEDLINE 96064693  
 EM 199512  
 ED Entered STN: 19960126  
 Last Updated on STN: 19970509

L5 ANSWER 16 OF 38 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 1994:678838 CAPLUS  
 DN 121:278838  
 TI Assays and therapeutic methods based on lymphocyte chemoattractants  
 IN Springer, Timothy A.; Roth, Stephen J.; Carr, Michelle W.  
 PA Center for Blood Research, Inc., USA  
 SO PCT Int. Appl., 106 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9420142	A1	19940915	WO 1994-US2632	19940311 <--
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5514555	A	19960507	US 1993-30764	19930312
	AU 9464043	A1	19940926	AU 1994-64043	19940311 <--
	JP 08507860	T2	19960820	JP 1994-520322	19940311
PRAI	US 1993-30764		19930312		
	WO 1994-US2632		19940311		

L5 ANSWER 17 OF 38 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 1994:550548 CAPLUS  
 DN 121:150548  
 TI C-C CKR-1, C-C chemokine \*\*\*receptor\*\*\*  
 IN Horuk, Richard; Neote, Kuldeep; Schall, Thomas  
 PA Genentech, Inc., USA  
 SO PCT Int. Appl., 90 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9411504	A1	19940526	WO 1993-US10672	19931104 <--
	W: CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE  
JP 08503463 T2 19960416 JP 1993-512228 19931104  
PRAI US 1992-974025 19921110  
WO 1993-US10672 19931104

L5 ANSWER 18 OF 38 DRUGNL COPYRIGHT 2003 IMSWoRLD on STN

ACCESSION NUMBER: 94:622 DRUGNL  
TITLE: Novel Approaches to Inflammation Intervention at LeukoSite  
SOURCE: R&D Focus Drug News ( \*\*\*13 Jun 1994\*\*\* ).  
WORD COUNT: 504

L5 ANSWER 19 OF 38 PHIN COPYRIGHT 2003 PJB on STN

AN 95:15282 PHIN  
DN S00456962  
DED 29 Aug 1995  
TI Warner-Lambert extends LeukoSite agreement  
SO Scrip ( \*\*\*1995\*\*\* ) No. 2055 p23  
DT Newsletter  
FS FULL

L5 ANSWER 20 OF 38 PROMT COPYRIGHT 2003 Gale Group on STN

ACCESSION NUMBER: 95:41517 PROMT  
TITLE: Melanoma Tx May Be a Few Years Away  
Melanoma treatment progress made with advances in  
microbiology & immunology  
SOURCE: Dermatology Times, ( \*\*\*Jan 1995\*\*\* ) pp. 1.  
ISSN: 0196-6197.  
LANGUAGE: English  
WORD COUNT: 696  
\*FULL TEXT IS AVAILABLE IN THE ALL FORMAT\*

L5 ANSWER 21 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 95:738805 SCISEARCH  
GA The Genuine Article (R) Number: TB163  
TI A DISTINCT PATTERN OF CYTOKINE GENE-EXPRESSION BY HUMAN CD83(+) BLOOD  
DENDRITIC CELLS  
AU ZHOU L J; TEDDER T F (Reprint)  
CS DUKE UNIV, MED CTR, DEPT IMMUNOL, BOX 3010, 353 JONES BLDG, RES DR,  
DURHAM, NC, 27710 (Reprint); DUKE UNIV, MED CTR, DEPT IMMUNOL, DURHAM, NC,  
27710  
CYA USA  
SO BLOOD, ( \*\*\*01 NOV 1995\*\*\* ) Vol. 86, No. 9, pp. 3295-3301.  
ISSN: 0006-4971.  
DT Note; Journal  
FS LIFE; CLIN  
LA ENGLISH  
REC Reference Count: 25  
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 22 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 95:136628 SCISEARCH  
GA The Genuine Article (R) Number: QF778  
TI DIFFERENTIAL-EFFECTS OF ANTIINFLAMMATORY CYTOKINES (IL-4, IL-10 AND IL-13)  
ON TUMORICIDAL AND CHEMOTACTIC PROPERTIES OF HUMAN MONOCYTES INDUCED BY  
MONOCYTE CHEMOTACTIC AND ACTIVATING FACTOR  
AU YANO S; SONE S (Reprint); NISHIOKA Y; MUKAIDA N; MATSUSHIMA K; OGURA T  
CS UNIV TOKUSHIMA, SCH MED, DEPT INTERNAL MED 3, KURAMOTO CHO 3, TOKUSHIMA  
770, JAPAN (Reprint); UNIV TOKUSHIMA, SCH MED, DEPT INTERNAL MED 3,  
TOKUSHIMA 770, JAPAN; KANAZAWA UNIV, SCH MED, CANC RES INST, DEPT  
PHARMACOL, KANAZAWA, ISHIKAWA 920, JAPAN  
CYA JAPAN  
SO JOURNAL OF LEUKOCYTE BIOLOGY, ( \*\*\*FEB 1995\*\*\* ) Vol. 57, No. 2, pp.  
303-309.  
ISSN: 0741-5400.  
DT Article; Journal  
FS LIFE  
LA ENGLISH  
REC Reference Count: 35  
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 23 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 95:30460 SCISEARCH

TI \*\*\*MCP\*\*\* - \*\*\*1\*\*\* -STIMULATED MONOCYTE ATTACHMENT TO LAMININ IS  
 MEDIATED BY BETA(2)-INTEGRINS  
 AU JIANG Y L; ZHU J F; LUSCINSKAS F W; GRAVES D T (Reprint)  
 CS BOSTON UNIV, MED CTR, SCH GRAD DENT, DEPT ORAL BIOL, RM W215, 700 ALBANY  
 ST, BOSTON, MA, 02118 (Reprint); BOSTON UNIV, MED CTR, SCH GRAD DENT, DEPT  
 ORAL BIOL, BOSTON, MA, 02118; BOSTON UNIV, SCH MED, DEPT BIOCHEM, BOSTON,  
 MA, 02118; BRIGHAM & WOMENS HOSP, DEPT PATHOL, DIV VASC RES, BOSTON, MA,  
 02115; HARVARD UNIV, SCH MED, BOSTON, MA, 02115  
 CYA USA  
 SO AMERICAN JOURNAL OF PHYSIOLOGY-CELL PHYSIOLOGY, ( \*\*\*OCT 1994\*\*\* ) Vol.  
 36, No. 4, pp. C1112-C1118.  
 ISSN: 0363-6143.  
 DT Article; Journal  
 FS LIFE  
 LA ENGLISH  
 REC Reference Count: 30  
 \*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 24 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN  
 AN 94:723204 SCISEARCH  
 GA The Genuine Article (R) Number: PQ410  
 TI BCG-INDUCED GRANULOMA-FORMATION IN MURINE TISSUES  
 AU GORDON S (Reprint); KESHAV S; STEIN M  
 CS UNIV OXFORD, SIR WILLIAM DUNN SCH PATHOL, S PARKS RD, OXFORD OX1 3RE,  
 ENGLAND (Reprint)  
 CYA ENGLAND  
 SO IMMUNOBIOLOGY, ( \*\*\*OCT 1994\*\*\* ) Vol. 191, No. 4-5, pp. 369-377.  
 ISSN: 0171-2985.  
 DT Article; Journal  
 FS LIFE  
 LA ENGLISH  
 REC Reference Count: 15  
 \*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 25 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN  
 AN 94:707806 SCISEARCH  
 GA The Genuine Article (R) Number: PP613  
 TI GENE-EXPRESSION OF MONOCYTE CHEMOATTRACTANT PROTEIN-1 IN HUMAN MONOCYTES  
 IS REGULATED BY CELL-DENSITY THROUGH PROTEIN-TYROSINE KINASE AND  
 PROTEIN-KINASE-C  
 AU ZEN K; MASUDA J (Reprint); SASAGURI T; KOSAKA C; OGATA J  
 CS NATL CARDIOVASC CTR, RES INST, 5-7-1 FIJSHIRO DAI, SUITA, OSAKA 565, JAPAN  
 (Reprint); NATL CARDIOVASC CTR, RES INST, SUITA, OSAKA 565, JAPAN  
 CYA JAPAN  
 SO EXPERIMENTAL CELL RESEARCH, ( \*\*\*NOV 1994\*\*\* ) Vol. 215, No. 1, pp.  
 172-179.  
 ISSN: 0014-4827.  
 DT Article; Journal  
 FS LIFE  
 LA ENGLISH  
 REC Reference Count: 52  
 \*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 26 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN  
 AN 93:180982 SCISEARCH  
 GA The Genuine Article (R) Number: KR934  
 TI EXPRESSION OF CSF-1, C-FMS, AND \*\*\*MCP\*\*\* - \*\*\*1\*\*\* IN THE  
 CENTRAL-NERVOUS-SYSTEM OF RATS WITH EXPERIMENTAL ALLERGIC  
 ENCEPHALOMYELITIS  
 AU HULKOWER K; BROSNAN C F; AQUINO D A; CAMMER W; KULSHRESTHA S; GUIDA M P;  
 RAPOPORT D A; BERMAN J W (Reprint)  
 CS YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT PATHOL, 1300 MORRIS PK AVE,  
 BRONX, NY, 10461; YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT NEUROSCI,  
 BRONX, NY, 10461; YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT NEUROL,  
 BRONX, NY, 10461; YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT MICROBIOL &  
 IMMUNOL, BRONX, NY, 10461  
 CYA USA  
 SO JOURNAL OF IMMUNOLOGY, ( \*\*\*15 MAR 1993\*\*\* ) Vol. 150, No. 6, pp.  
 2525-2533.  
 ISSN: 0022-1767.  
 DT Article; Journal  
 FS LIFE  
 LA ENGLISH  
 REC Reference Count: 64  
 \*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 27 OF 38 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN  
 AN 91:690317 SCISEARCH  
 GA The Genuine Article (R) Number: GU967  
 TI MONOCYTE TRANSMIGRATION INDUCED BY MODIFICATION OF LOW-DENSITY-LIPOPROTEIN  
 IN COCULTURES OF HUMAN AORTIC-WALL CELLS IS DUE TO INDUCTION OF MONOCYTE  
 CHEMOTACTIC PROTEIN-1 SYNTHESIS AND IS ABOLISHED BY HIGH-DENSITY-  
 LIPOPROTEIN  
 AU NAVAB M (Reprint); IMES S S; HAMA S Y; HOUGH G P; ROSS L A; BORK R W;  
 VALENTE A J; BERLINER J A; DRINKWATER D C; LAKS H; FOGELMAN A M  
 CS UNIV CALIF LOS ANGELES, CTR HLTH SCI, SCH MED, DEPT MED, DIV CARDIOL, ROOM  
 47-123, LOS ANGELES, CA, 90024 (Reprint); UNIV CALIF LOS ANGELES, SCH MED,  
 DEPT MED, DIV HEMATOL ONCOL, LOS ANGELES, CA, 90024; UNIV CALIF LOS  
 ANGELES, SCH MED, DEPT PATHOL, LOS ANGELES, CA, 90024; UNIV CALIF LOS  
 ANGELES, SCH MED, DEPT OTOLARYNGOL HEAD & NECK SURG, LOS ANGELES, CA,  
 90024; UNIV TEXAS, DEPT PATHOL, SAN ANTONIO, TX, 78284  
 CYA USA  
 SO JOURNAL OF CLINICAL INVESTIGATION, ( \*\*\*1991\*\*\* ) Vol. 88, No. 6, pp.  
 2039-2046.  
 DT Article; Journal  
 FS LIFE  
 LA ENGLISH  
 REC Reference Count: 43  
 \*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

L5 ANSWER 28 OF 38 USPATFULL on STN  
 AN 2000:138077 USPATFULL  
 TI Recombinant mammalian monocyte chemotactic protein-1 ( \*\*\*MCP\*\*\* -  
 \*\*\*1\*\*\* ) \*\*\*receptors\*\*\* (MCP-1R, CCR-2)  
 IN Charo, Israel F., Lafayette, CA, United States  
 Coughlin, Shaun R., Tiburon, CA, United States  
 PA The Regents of the University of California, Oakland, CA, United States  
 (U.S. corporation)  
 PI US 6132987 20001017  
 WO 9519436 19950720  
 AI US 1995-446669 19950525 (8)  
 WO 1995-US476 19950111  
 19950525 PCT 371 date  
 19950525 PCT 102(e) date  
 RLI Continuation-in-part of Ser. No. US 1994-182962, filed on 13 Jan 1994,  
 now abandoned  
 DT Utility  
 FS Granted  
 LN.CNT 2431  
 INCL INCLM: 435/069.100  
 INCLS: 536/023.500; 530/350.000; 514/002.000; 435/320.100; 435/325.000;  
 435/252.300; 435/254.110; 435/007.100; 435/007.210; 435/348.000  
 NCL NCLM: 435/069.100  
 NCLS: 435/007.100; 435/007.210; 435/252.300; 435/254.110; 435/320.100;  
 435/325.000; 435/348.000; 514/002.000; 530/350.000; 536/023.500  
 IC [7]  
 ICM: C12N015-12  
 ICS: C07K014-715; G01N033-53  
 EXF 536/23.5; 530/350; 435/69.1; 435/320.1; 435/325; 435/252.3; 435/254.4;  
 435/7.1; 435/7.21; 435/348; 514/1; 514/2  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 29 OF 38 USPATFULL on STN  
 AN 1999:163409 USPATFULL  
 TI Functional expression of mammalian adenylyl cyclase in yeast  
 IN Broach, James R., Princeton, NJ, United States  
 Manfredi, John P., Ossining, NY, United States  
 Trueheart, Joshua, Nyack, NY, United States  
 PA Cadus Pharmaceutical Corporation, Tarrytown, NY, United States (U.S.  
 corporation)  
 PI US 6001553 19991214  
 WO 9530012 19951109 <--  
 AI US 1997-732218 19970114 (8)  
 WO 1995-US5149 19950426  
 19970114 PCT 371 date  
 19970114 PCT 102(e) date  
 RLI Continuation-in-part of Ser. No. US 1994-233700, filed on 26 Apr 1994,  
 now abandoned  
 DT Utility  
 FS Granted  
 LN.CNT 4954



NCL INCLS: 435/252.200; 435/254.210; 435/232.000  
NCLM: 435/004.000  
NCLS: 435/232.000; 435/252.200; 435/254.210  
IC [6]  
ICM: C12Q001-00  
ICS: C12N001-14; C12N009-88  
EXF 435/4; 435/252.2; 435/254.21; 435/232  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 30 OF 38 USPATFULL on STN  
AN 1999:155198 USPATFULL  
TI Agents for inhibition of chemoattractant  
IN Williams, Timothy J., London, United Kingdom  
Jose, Peter J., London, United Kingdom  
Griffiths-Johnson, David A., London, United Kingdom  
Hsuan, John J., London, United Kingdom  
PA Imperial College of Science, Technology & Medicine, London, United  
Kingdom (non-U.S. corporation)  
PI US 5993814 19991130  
WO 9507985 19950323 <--  
AI US 1996-615232 19960813 (8)  
WO 1994-GB2006 19940914  
19960813 PCT 371 date  
19960813 PCT 102(e) date  
PRAI GB 1993-18984 19930912  
GB 1994-8602 19940429  
DT Utility  
FS Granted  
LN.CNT 1110  
INCL INCLM: 424/145.100  
INCLS: 530/387.100; 530/387.900; 514/002.000; 514/008.000; 514/012.000;  
514/885.000; 424/139.100  
NCL NCLM: 424/145.100  
NCLS: 424/139.100; 514/002.000; 514/008.000; 514/012.000; 514/885.000;  
530/387.100; 530/387.900  
IC [6]  
ICM: C07K016-24  
ICS: A61K039-395  
EXF 530/350; 530/387.1; 530/387.9; 514/2; 514/8; 514/12; 514/885; 424/139.1;  
424/145.1  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 31 OF 38 USPATFULL on STN  
AN 1998:147246 USPATFULL  
TI Granulocyte chemotactic protein  
IN Van Damme, Jo, Brussels, Belgium  
Proost, Paul, Heverlee, Belgium  
PA Stichting Rega vzw, Leuven, Belgium (non-U.S. corporation)  
PI US 5840524 19981124  
WO 9412537 19940609 <--  
AI US 1995-436420 19950524 (8)  
WO 1993-EP3330 19931126  
19950524 PCT 371 date  
19950524 PCT 102(e) date  
DT Utility  
FS Granted  
LN.CNT 1183  
INCL INCLM: 435/069.100  
INCLS: 530/300.000; 530/324.000; 536/023.100  
NCL NCLM: 435/069.100  
NCLS: 530/300.000; 530/324.000; 536/023.100  
IC [6]  
ICM: C12P021-06  
ICS: A61K038-00; C07H021-04  
EXF 435/69.1; 530/300; 530/324; 536/23.1  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 32 OF 38 USPATFULL on STN  
AN 1998:36596 USPATFULL  
TI Envelope fusion vectors for use in gene delivery  
IN Paul, Ralph W., Seattle, WA, United States  
Overell, Robert, Seattle, WA, United States  
PA Targeted Genetics Corporation, Seattle, WA, United States (U.S.  
corporation)  
PI US 5736387 19980407

AI US 1994-244469 19940601 (8)  
 WO 1995-US9406128 19950601  
 19940601 PCT 371 date  
 19940601 PCT 102(e) date

RLI Continuation-in-part of Ser. No. US 1993-70117, filed on 1 Jun 1993, now abandoned

DT Utility  
 FS Granted  
 LN.CNT 2097

INCL INCLM: 435/320.100  
 INCLS: 435/325.000; 435/069.700; 435/069.500; 435/069.510; 435/069.520;  
 435/091.200; 435/006.000; 424/093.210; 514/044.000; 530/387.100;  
 530/350.000; 536/023.500; 536/024.310

NCL NCLM: 435/320.100  
 NCLS: 424/093.210; 435/006.000; 435/069.500; 435/069.510; 435/069.520;  
 435/069.700; 435/091.200; 435/325.000; 514/044.000; 530/350.000;  
 530/387.100; 536/023.500; 536/024.310

IC [6]  
 ICM: C12N015-63

EXF 514/44; 424/93.21; 424/69.51; 424/69.52; 435/320.1; 435/6; 435/91.7;  
 435/325; 435/69.7; 435/69.52; 435/69.1; 435/69.5; 435/69.51; 435/91.2;  
 530/387.1; 530/350; 536/23.5

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 33 OF 38 USPATFULL on STN  
 AN 97:56494 USPATFULL  
 TI Method of marking a liquid  
 IN Slater, James Howard, 38 Heol-Y-Delyn, Lisvane, Cardiff CF4 5SR, Great Britain  
 Minton, John Edward, 2 Mill Place, Lisvane, Cardiff CF4 5TF, Great Britain

PI US 5643728 19970701  
 WO 9404918 19940303 <--

AI US 1995-392821 19950227 (8)  
 WO 1993-GB1822 19930826  
 19950227 PCT 371 date  
 19950227 PCT 102(e) date

PRAI GB 1992-18131 19920826  
 DT Utility  
 FS Granted  
 LN.CNT 1087

INCL INCLM: 435/006.000  
 INCLS: 435/004.000; 435/007.100; 435/015.000; 436/056.000; 436/057.000;  
 436/501.000; 436/518.000; 436/526.000; 436/527.000; 536/025.300

NCL NCLM: 435/006.000  
 NCLS: 435/004.000; 435/007.100; 435/015.000; 436/056.000; 436/057.000;  
 436/501.000; 436/518.000; 436/526.000; 436/527.000; 536/025.300

IC [6]  
 ICM: C07H021-00  
 ICS: C12Q001-68

EXF 435/6; 435/4; 435/7.1; 435/15; 436/501; 436/518; 436/526; 436/527;  
 436/56; 436/57; 935/77; 935/78; 514/44; 536/25.3

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 34 OF 38 USPATFULL on STN  
 AN 95:110431 USPATFULL  
 TI Method of inhibiting pro-inflammatory mediator release from basophils and mast cells  
 IN Kuna, Piotr, Port Jefferson, NY, United States  
 Kaplan, Allen P., St. James, NY, United States  
 PA The Research Foundation of State University of New York, Stony Brook, NY, United States (U.S. corporation)

PI US 5474983 19951212 <--

AI US 1993-31772 19930315 (8)  
 DT Utility  
 FS Granted  
 LN.CNT 852

INCL INCLM: 514/012.000  
 INCLS: 514/021.000

NCL NCLM: 514/012.000  
 NCLS: 514/021.000

IC [6]  
 ICM: A61K038-19

EXF 514/12; 514/21

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 35 OF 38 USPATFULL on STN  
 AN 95:94811 USPATFULL  
 TI Device and method for analysis of blood components and identifying  
 inhibitors and promoters of the inflammatory response  
 IN Springer, Timothy A., Chestnut Hill, MA, United States  
 Lawrence, Michael, Brookline, MA, United States  
 PA Center for Blood Research, Inc., Boston, MA, United States (U.S.  
 corporation)  
 PI US 5460945 19951024 <--  
 AI US 1992-887444 19920520 (7)  
 RLI Continuation-in-part of Ser. No. US 1991-707841, filed on 30 May 1991,  
 now abandoned  
 DT Utility  
 FS Granted  
 LN.CNT 3399  
 INCL INCLM: 435/007.240  
 INCLS: 422/058.000; 422/069.000; 427/002.110; 427/002.130; 435/002.000;  
 435/004.230; 435/007.800; 435/029.000; 435/030.000; 435/174.000;  
 435/176.000; 435/177.000; 435/240.200; 435/287.100; 435/287.200;  
 435/287.900; 435/288.300; 435/288.500  
 NCL NCLM: 435/007.240  
 NCLS: 422/058.000; 422/069.000; 427/002.110; 427/002.130; 435/002.000;  
 435/007.230; 435/007.800; 435/029.000; 435/030.000; 435/174.000;  
 435/176.000; 435/177.000; 435/287.100; 435/287.200; 435/287.900;  
 435/288.300; 435/288.500; 435/379.000  
 IC [6]  
 ICM: C12N005-00  
 ICS: C12Q001-02; G01N033-566  
 EXF 422/69; 422/58; 427/2; 435/2; 435/7.23; 435/7.24; 435/7.8; 435/29;  
 435/30; 435/174; 435/176; 435/177; 435/287; 435/240.2; 436/503  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 36 OF 38 USPATFULL on STN  
 AN 95:92775 USPATFULL  
 TI Human monocyte chemoattractant protein-1 ( \*\*\*MCP\*\*\* - \*\*\*1\*\*\* )  
 derivatives  
 IN Rollins, Barrett, Brookline, MA, United States  
 Zhang, Yu J., Brookline, MA, United States  
 PA Dana-Farber Cancer Institute, Boston, MA, United States (U.S.  
 corporation)  
 PI US 5459128 19951017 <--  
 AI US 1994-330218 19941027 (8)  
 RLI Continuation-in-part of Ser. No. US 1993-152301, filed on 12 Nov 1993,  
 now abandoned  
 DT Utility  
 FS Granted  
 LN.CNT 400  
 INCL INCLM: 514/008.000  
 INCLS: 514/012.000; 514/021.000; 530/351.000; 530/395.000; 530/402.000;  
 530/409.000; 424/085.100  
 NCL NCLM: 514/008.000  
 NCLS: 424/085.100; 514/012.000; 514/021.000; 530/351.000; 530/395.000;  
 530/402.000; 530/409.000  
 IC [6]  
 ICM: C07K014-52  
 ICS: C08H001-00; A61K038-19; A61K045-05  
 EXF 530/350; 530/351; 530/395; 530/402; 530/409; 514/8; 514/12; 514/21;  
 424/85.1; 930/140; 930/141  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 37 OF 38 USPATFULL on STN  
 AN 95:71471 USPATFULL  
 TI \*\*\*Antibodies\*\*\* to human IL-8 type B \*\*\*receptor\*\*\*  
 IN Chuntharapai, Anan, 460 Point San Bruno Blvd., South San Francisco, CA,  
 United States 94080  
 Hebert, Caroline, 460 Point San Bruno Blvd., South San Francisco, CA,  
 United States 94080  
 Kim, Kyung J., 460 Point San Bruno Blvd., South San Francisco, CA,  
 United States 94080  
 Lee, James, 460 Point San Bruno Blvd., South San Francisco, CA, United  
 States 94080  
 PI US 5440021 19950808 <--  
 AI US 1994-202056 19940225 (8)  
 RLI Continuation-in-part of Ser. No. US 1991-677211, filed on 29 Mar 1991,  
 now abandoned

FS Granted  
LN.CNT 2693  
INCL INCLM: 530/388.220  
INCLS: 530/388.230; 530/389.100; 530/389.200; 435/240.270  
NCL NCLM: 530/388.220  
NCLS: 530/388.230; 530/389.100; 530/389.200  
IC [6]  
ICM: C07K016-28  
ICS: C07K016-24; C12N005-22  
EXF 424/158.1; 530/388.73; 530/388.23; 530/389.2; 530/388.33; 530/389.1;  
435/240.27

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 38 OF 38 USPATFULL on STN  
AN 95:67213 USPATFULL  
TI Use of platelet factor 4 to treat inflammatory diseases  
IN Kuna, Piotr, Port Jefferson, NY, United States  
Kaplan, Allen P., St. James, NY, United States  
PA The Research Foundation of State University of New York, Albany, NY,  
United States (U.S. corporation)  
PI US 5436222 19950725 <--  
AI US 1993-31773 19930315 (8)  
DT Utility  
FS Granted  
LN.CNT 716  
INCL INCLM: 514/012.000  
INCLS: 530/300.000; 530/324.000; 514/826.000; 514/886.000  
NCL NCLM: 514/012.000  
NCLS: 514/826.000; 514/886.000; 530/300.000; 530/324.000  
IC [6]  
ICM: A61K038-00  
ICS: A61K038-02; C07K005-00; C07K007-00  
EXF 514/12; 514/826; 514/886; 530/300; 530/324; 435/69.1  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> S CCR2 AND antibody

27 FILES SEARCHED...

60 FILES SEARCHED...

L6 1233 CCR2 AND ANTIBODY

=> DUP REM L6

DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,  
DRUGLAUNCH, DRUGMONOG2, DRUGUPDATES, FEDRIP, FOREGE, GENBANK, KOSMET,  
MEDICONF, NUTRACEUT, PCTGEN, PHAR, PHARMAML, RDISCLOSURE, SYNTHLINE'.

ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE

PROCESSING IS APPROXIMATELY 97% COMPLETE FOR L6

PROCESSING COMPLETED FOR L6

L7 682 DUP REM L6 (551 DUPLICATES REMOVED)

=> S L7 AND PY<=1995

'1995' NOT A VALID FIELD CODE

6 FILES SEARCHED...

9 FILES SEARCHED...

13 FILES SEARCHED...

17 FILES SEARCHED...

'1995' NOT A VALID FIELD CODE

30 FILES SEARCHED...

'1995' NOT A VALID FIELD CODE

'1995' NOT A VALID FIELD CODE

41 FILES SEARCHED...

'1995' NOT A VALID FIELD CODE

46 FILES SEARCHED...

49 FILES SEARCHED...

'1995' NOT A VALID FIELD CODE

57 FILES SEARCHED...

60 FILES SEARCHED...

L8 1 L7 AND PY<=1995

=> D L8

L8 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1988:35083 BIOSIS

DN PREV198885022808; BA85:22808

TI RABBIT NEPHROTOXIC NEPHRITIS EFFECT OF A THROMBOXANE SYNTHETASE INHIBITOR

AU SHINKAI Y [Reprint author]; CAMERON J S  
CS CLINICAL SCI LAB, 17TH FLOOR GUY'S TOWER, GUY'S HOSP, LONDON SE1 9RT, UK  
SO Nephron, (1987) Vol. 47, No. 3, pp. 211-219.  
CODEN: NPRNAY. ISSN: 0028-2766.  
DT Article  
FS BA  
LA ENGLISH  
ED Entered STN: 28 Dec 1987  
STN INTERNATIONAL LOGOFF AT 12:05:23 ON 02 DEC 2003

OM protein - protein search, using sw model

Run on: November 25, 2003, 23:18:24 ; Search time 21 Seconds  
 (without alignments)  
 725.329 Million cell updates/sec

Title: US-09-625-573-4  
 Perfect score: 1900  
 Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1900	100.0	360	1	US-08-450-393A-4	Sequence 4, Appli
2	1900	100.0	360	3	US-08-446-669-4	Sequence 4, Appli
3	1900	100.0	360	3	US-09-045-583-50	Sequence 50, Appl
4	1900	100.0	360	4	US-09-534-185-50	Sequence 50, Appl
5	1900	100.0	360	5	PCT-US95-00476-4	Sequence 4, Appli
6	1873	98.6	360	4	US-08-833-752-7	Sequence 7, Appli
7	1849	97.3	360	3	US-09-045-583-51	Sequence 51, Appl
8	1849	97.3	360	4	US-09-534-185-51	Sequence 51, Appl
9	1838	96.7	347	1	US-08-461-244-3	Sequence 3, Appli
10	1651.5	86.9	374	1	US-08-450-393A-2	Sequence 2, Appli
11	1651.5	86.9	374	3	US-08-446-669-2	Sequence 2, Appli

12	1651.5	86.9	374	5	PCT-US95-00476-2	Sequence 2, Appli
13	1568.5	82.6	344	3	US-08-466-343D-9	Sequence 9, Appli
14	1473	77.5	329	4	US-09-502-783A-9	Sequence 9, Appli
15	1386	72.9	354	4	US-08-724-984A-2	Sequence 2, Appli
16	1371	72.2	352	4	US-09-517-605-5	Sequence 5, Appli
17	1370	72.1	352	3	US-09-045-583-52	Sequence 52, Appl
18	1370	72.1	352	4	US-09-534-185-52	Sequence 52, Appl
19	1364	71.8	352	3	US-09-087-232A-13	Sequence 13, Appl
20	1364	71.8	352	3	US-08-861-105-14	Sequence 14, Appl
21	1364	71.8	352	3	US-08-575-967A-2	Sequence 2, Appli
22	1364	71.8	352	4	US-08-833-752-5	Sequence 5, Appli
23	1364	71.8	352	4	US-09-796-202-1	Sequence 1, Appli
24	1356	71.4	352	4	US-09-502-783A-2	Sequence 2, Appli
25	1355	71.3	352	3	US-08-466-343D-2	Sequence 2, Appli
26	1036	54.5	355	1	US-08-012-988A-2	Sequence 2, Appli
27	1036	54.5	355	1	US-08-450-393A-5	Sequence 5, Appli
28	1036	54.5	355	3	US-08-446-669-5	Sequence 5, Appli
29	1036	54.5	355	4	US-09-239-938-1	Sequence 1, Appli
30	1036	54.5	355	4	US-09-886-319A-14	Sequence 14, Appl
31	1036	54.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
32	1008	53.1	355	4	US-08-833-752-9	Sequence 9, Appli
33	981	51.6	355	3	US-09-045-583-53	Sequence 53, Appl
34	981	51.6	355	4	US-09-534-185-53	Sequence 53, Appl
35	960.5	50.6	355	4	US-09-886-319A-13	Sequence 13, Appl
36	958	50.4	355	4	US-08-720-565-2	Sequence 2, Appli
37	947	49.8	355	3	US-08-575-967A-4	Sequence 4, Appli
38	947	49.8	355	3	US-08-847-296B-1	Sequence 1, Appli
39	947	49.8	355	3	US-09-045-583-54	Sequence 54, Appl
40	947	49.8	355	4	US-09-534-185-54	Sequence 54, Appl
41	947	49.8	355	4	US-08-720-565-4	Sequence 4, Appli
42	940.5	49.5	356	4	US-08-567-882-7	Sequence 7, Appli
43	917	48.3	355	4	US-08-833-752-8	Sequence 8, Appli
44	916	48.2	355	4	US-08-720-565-6	Sequence 6, Appli
45	862.5	45.4	360	3	US-08-875-573-20	Sequence 20, Appl

# ALIGNMENTS

RESULT 1

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

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Query Match          100.0%; Score 1900; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.9e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKCLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKCLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NP I IYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      |||
Db    301 NP I IYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

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RESULT 2
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987

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; GENERAL INFORMATION:
;   APPLICANT:  Charo, Israel
;   APPLICANT:  Coughlin, Shaun
;   TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;   TITLE OF INVENTION:  PROTEIN RECEPTORS
;   NUMBER OF SEQUENCES:  14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;     STREET:    5 Palo Alto Square
;     CITY:      Palo Alto
;     STATE:     California
;     COUNTRY:   USA
;     ZIP:       94306-2155
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/446,669
;     FILING DATE:       May 25, 1995
;     CLASSIFICATION:    435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:             Neeley, Richard
;     REGISTRATION NUMBER:  30,092
;     REFERENCE/DOCKET NUMBER:  UCAL-237/01US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:        415-843-5000
;     TELEFAX:          415-857-0663
;     TELEX:            380816CooleyPA
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:        360 amino acids
;       TYPE:           amino acid
;       TOPOLOGY:      linear
;       MOLECULE TYPE:  protein
US-08-446-669-4

```

```

Query Match          100.0%;  Score 1900;  DB 3;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 3.9e-151;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120
        |||
Db     61 MLVVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240

```

```

Qy      241 AVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

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RESULT 3

US-09-045-583-50

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; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
;   APPLICANT:  Graham, Gerard J. et al.
;   TITLE OF INVENTION:  No. 6287805el Molecules of the G Protein-Coupled
;   NUMBER OF SEQUENCES:  56
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;     STREET:    28 State Street
;     CITY:      Boston
;     STATE:     Massachusetts
;     COUNTRY:   USA
;     ZIP:       02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/045,583
;     FILING DATE:       20-MAR-98
;     CLASSIFICATION:    435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Mandragouras, Amy E.
;     REGISTRATION NUMBER:  36,207
;     REFERENCE/DOCKET NUMBER:  MNI-044
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (617)227-7400
;     TELEFAX:   (617)742-4214
;   INFORMATION FOR SEQ ID NO:  50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  360 amino acids
;       TYPE:    amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-09-045-583-50

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Query Match          100.0%;  Score 1900;  DB 3;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 3.9e-151;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSA	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSA	360

# RESULT 4

US-09-534-185-50

; Sequence 50, Application US/09534185

; Patent No. 6403767

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
; Heptahelical Receptor Superfamily and Uses  
; Therefor

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/534,185

; FILING DATE: 24-Mar-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/045,583

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

```

; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

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Query Match          100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.9e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

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# RESULT 5

PCT-US95-00476-4

; Sequence 4, Application PC/TUS9500476

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Robbins, Berliner & Carson

; STREET: 201 N. Figueroa Street, 5th Floor

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

```

;      ZIP: 90012-2628
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: PCT/US95/00476
;      FILING DATE:
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Berliner, Robert
;      REGISTRATION NUMBER: 20,121
;      REFERENCE/DOCKET NUMBER: 5555-291
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 310-977-1001
;      TELEFAX: 310-977-1003
;      TELEX:
;      INFORMATION FOR SEQ ID NO: 4:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 360 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
PCT-US95-00476-4

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Query Match          100.0%; Score 1900; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.9e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKCLKLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKCLKLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NP I IYAFVGEKFRRYLSVFFRKHI TKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NP I IYAFVGEKFRRYLSVFFRKHI TKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360

```



```

Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240
QY      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQAIQVTETLGMTHCCI 300
QY      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
        ||||||||||||||||:||||||| ||||||||||||||||||||||||||||
Db      301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

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RESULT 7

US-09-045-583-51

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; Sequence 51, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
;   APPLICANT:  Graham, Gerard J. et al.
;   TITLE OF INVENTION:  No. 6287805e1 Molecules of the G Protein-Coupled
;   NUMBER OF SEQUENCES:  56
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;     STREET:    28 State Street
;     CITY:      Boston
;     STATE:     Massachusetts
;     COUNTRY:   USA
;     ZIP:       02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/045,583
;     FILING DATE:       20-MAR-98
;     CLASSIFICATION:    435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Mandragouras, Amy E.
;     REGISTRATION NUMBER:  36,207
;     REFERENCE/DOCKET NUMBER:  MNI-044
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (617)227-7400
;     TELEFAX:   (617)742-4214
;   INFORMATION FOR SEQ ID NO:  51:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  360 amino acids
;       TYPE:    amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-09-045-583-51

```

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Query Match          97.3%;  Score 1849;  DB 3;  Length 360;
Best Local Similarity 97.2%;  Pred. No. 7.1e-147;
Matches 350;  Conservative 5;  Mismatches 5;  Indels 0;  Gaps 0;

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Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60  
 |||  
 Db 1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 |||  
 Db 61 MLVVLILINCKKLKSLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 |||  
 Db 121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240  
 ||: |||: |||  
 Db 181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 ||: |||  
 Db 241 AVRLIPTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVIFYRETVDGVTSTNTPSTGEQEV SAGL 360  
 |||: |||: |||  
 Db 301 NPIIYAFVGEKFRRYLSMFFRKYITKRFCQCPVIFYRETVDGVTSTNTPSTAEQEV SAGL 360

RESULT 8

US-09-534-185-51

; Sequence 51, Application US/09534185

; Patent No. 6403767

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6403767e1 Molecules of the G Protein-Coupled  
 ; Heptahelical Receptor Superfamily and Uses  
 ; Therefor

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/534,185

; FILING DATE: 24-Mar-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/045,583

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.



```

;      REGISTRATION NUMBER: 36,207
;      REFERENCE/DOCKET NUMBER: MNI-044
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (617)227-7400
;      TELEFAX: (617)742-4214
;      INFORMATION FOR SEQ ID NO: 51:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 360 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FRAGMENT TYPE: internal
;      SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

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Query Match          97.3%;  Score 1849;  DB 4;  Length 360;
Best Local Similarity 97.2%;  Pred. No. 7.1e-147;
Matches 350;  Conservative 5;  Mismatches 5;  Indels 0;  Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKCLKLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKCLKSLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYLGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240
      |||
Db    181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRLIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQKCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      |||
Db    301 NPIIYAFVGEKFRRYLSMFFRKYITKRFCQKCPVFYRETVDGVTSTNTPSTAEQEV SAGL 360

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# RESULT 9

US-08-461-244-3

; Sequence 3, Application US/08461244

; Patent No. 5776729

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Yi, Li

; APPLICANT: Ruben, Steven M.

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,



Db 301 RYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 347

RESULT 10

US-08-450-393A-2

; Sequence 2, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cserr, Luann  
; REGISTRATION NUMBER: 31,822  
; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663  
; TELEX: 380816CooleyPA  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-450-393A-2

Query Match 86.9%; Score 1651.5; DB 1; Length 374;  
Best Local Similarity 95.5%; Pred. No. 2.2e-130;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI	FGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI	FGFVGN	60
Qy	61	MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY		120
Db	61	MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY		120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNI LGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNI LGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240  
 Qy 241 AVRVI FTIMIVYFLFWTPYNI VIL LNTFQE FFGLSNCESTS QLDQATQVTETLGMTHCCI 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 AVRVI FTIMIVYFLFWTPYNI VIL LNTFQE FFGLSNCESTS QLDQATQVTETLGMTHCCI 300  
 Qy 301 NP I IYAFVGEKFR RYLSVFFRK HITKR FCKQCPV 334  
 ||||||||||||| :| || :| :|  
 Db 301 NP I IYAFVGEKFR ---SLF---HIALG-CRIAPL 327

RESULT 11

US-08-446-669-2

; Sequence 2, Application US/08446669

; Patent No. 6132987

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5000

; TELEFAX: 415-857-0663

; TELEX: 380816CooleyPA

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 374 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-446-669-2

Query Match 86.9%; Score 1651.5; DB 3; Length 374;  
Best Local Similarity 95.5%; Pred. No. 2.2e-130;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLI LINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLI LINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NP I IYAFVGEKFRRYLSVFFRKHITKR FCKQCPV 334
        |||
Db    301 NP I IYAFVGEKFR---SLF---HIALG-CRIAPL 327
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RESULT 12

PCT-US95-00476-2

; Sequence 2, Application PC/TUS9500476

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Robbins, Berliner & Carson

; STREET: 201 N. Figueroa Street, 5th Floor

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90012-2628

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/00476

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Berliner, Robert

```

;     REGISTRATION NUMBER: 20,121
;     REFERENCE/DOCKET NUMBER: 5555-291
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 310-977-1001
;     TELEFAX: 310-977-1003
;     TELEX:
;     INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 374 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
PCT-US95-00476-2

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Query Match          86.9%;  Score 1651.5;  DB 5;  Length 374;
Best Local Similarity 95.5%;  Pred. No. 2.2e-130;
Matches 319;  Conservative 3;  Mismatches 5;  Indels 7;  Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Qy     61 MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334
        ||||||||||||  |:|  ||  |:  |:
Db    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

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RESULT 13

US-08-466-343D-9

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; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDG NR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC

```

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; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-9

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Query Match          82.6%; Score 1568.5; DB 3; Length 344;
Best Local Similarity 95.3%; Pred. No. 1.7e-123;
Matches 302; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
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Db      1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
      |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy     138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
      |||
Db     121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy     198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
      |||
Db     181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      |||
Db     241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR---S 297

Qy     318 VFFRKHITKRFCQCPV 334
      :|  ||  |:  |:
Db     298 LF---HIALG-CRIAPL 310

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; TITLE OF INVENTION: No. 6388055e1 Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CKR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-724-984A-2

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Query Match          72.9%; Score 1386; DB 4; Length 354;
Best Local Similarity 74.0%; Pred. No. 3e-108;
Matches 259; Conservative 33; Mismatches 52; Indels 6; Gaps 2;

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Qy      17 GEEVTTFFDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLLK 74
      |  |  :| ||| ||| | :||| ||||| ||||| |||:| |||:||||
Db      5 GSVPTYIYDIDYGMSAPCQKINVKQIAAQLLPPLYSLVFIFGFAGNMMVFLILISCKKLLK 64

Qy      75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL 134
      :||| ||||| ||||| :||| ||| ||||| :||| |||: |||: ||||| |||||
Db      65 SVTDIYLLNLAISDLLFLLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFFIILL 124

Qy     135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF 194
      ||||| ||||| ||| ||| |||: |||: ||||| :||| |||: |||: ||||| |||||
Db     125 TIDRYLAIVHAVFALKVTTVNFGVITSVVTWVAVFASLPEIIFTRSQKEGFHYTCSPHF 184

Qy     195 PRG---WNNFHTIMRNILGLVLPLLMVICYSGILKTLRLRCRNEKKRHRRAVRVIFTIMI 250
      |  |  :| | : ||| :|||: ||||| ||| ||||| ||||| :||| |||
Db     185 PHTQYHFWKSFQTLKMVILSLILPLLVMICYSGILHTLFRRCRNEKKRHRRAVRLIFAIMI 244

Qy     251 VYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE 310

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Db	245	VYFLFWTPYNIIVLLLTTFQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYAFVGE	304
Qy	311	KFRRLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSA	360
Db	305	KFRSYLSVFFRKHIVKRFCKRCSIFQQDNPDRVSSVYTRSTGEHEVSTGL	354

Search completed: November 25, 2003, 23:21:40  
Job time : 22 secs

OM protein - protein search, using sw model

Run on: November 25, 2003, 23:03:19 ; Search time 44 Seconds  
(without alignments)  
1298.672 Million cell updates/sec

Title: US-09-625-573-4  
Perfect score: 1900  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNTPSTGEQEVSAAGL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%						
No.	Score	Query	Match	Length	DB	ID	Description
1	1900	100.0	360	16	AAR79166		Human monocyte che
2	1900	100.0	360	18	AAW35833		Human monocyte che
3	1900	100.0	360	22	AAG80108		Human CCR2b protei
4	1900	100.0	360	22	AAU07614		Human wild-type CC
5	1900	100.0	360	24	ABP97725		Amino acid sequenc
6	1900	100.0	360	24	ABP81987		Human C-C chemokin
7	1899	99.9	360	22	AAU07613		Human CCR2-64I pol
8	1894	99.7	360	22	ABB56340		Non-endogenous hum
9	1651.5	86.9	374	16	AAR79165		Human monocyte che
10	1651.5	86.9	374	22	AAG80107		Human CCR2a protei
11	1568.5	82.6	344	23	ABG92881		Class I receptors
12	1473	77.5	329	22	AAB46859		Human MCP-1 recept
13	1473	77.5	329	23	ABB81055		Human MCP-1 recept
14	1386	72.9	354	19	AAW54037		Mouse CC-CKR5 prot
15	1371	72.2	352	22	AAG79089		Amino acid sequenc
16	1364	71.8	352	18	AAW27407		Human CCR5. Homo
17	1364	71.8	352	18	AAW27123		Human chemokine re
18	1364	71.8	352	18	AAW27125		Macaque chemokine
19	1364	71.8	352	19	AAW23835		Human CC chemokine
20	1364	71.8	352	20	AAW88232		HIV-1 co-receptor
21	1364	71.8	352	22	AAG80111		Human CCR5 protein
22	1364	71.8	352	22	AAB82948		Human HIV-1 co-rec
23	1364	71.8	352	22	AAB83354		Human CCR5 protein
24	1364	71.8	352	22	AAE04321		Human chemokine re
25	1364	71.8	352	23	ABB08343		Human chemokine (C
26	1364	71.8	352	23	AAM52828		Human CC chemokine
27	1364	71.8	352	24	ABP97728		Amino acid sequenc
28	1364	71.8	352	24	ABP81933		Human C-C chemokin
29	1364	71.8	439	20	AAU41280		Fusion protein con
30	1359.5	71.6	371	19	AAW23834		Human CC chemokine
31	1358	71.5	352	22	ABB56342		Non-endogenous hum
32	1358	71.5	352	23	AAM52829		Human CCR5 Gln 55
33	1356	71.4	352	22	AAE07039		Human G-protein ch
34	1356	71.4	352	22	AAE07048		Human G-protein ch
35	1356	71.4	352	22	AAB46858		Human HDGMR10 prot
36	1356	71.4	352	23	AAE25811		Human G-protein ch
37	1356	71.4	352	23	ABG70597		Human G-protein ch
38	1356	71.4	352	23	ABG92883		Human immunoglobul
39	1356	71.4	352	23	ABB81054		G-protein chemokin
40	1356	71.4	352	23	AAU97152		Human G-protein ch
41	1356	71.4	352	24	ABG75540		Human G-protein ch
42	1355	71.3	352	18	AAW07602		Human G-protein ch
43	1355	71.3	352	21	AAU80128		Human G-protein ch
44	1355	71.3	352	22	AAE07037		Human G-protein ch
45	1355	71.3	352	22	AAE07046		Human G-protein ch

# ALIGNMENTS

RESULT 1

AAR79166

ID AAR79166 standard; Protein; 360 AA.

XX

AC AAR79166;

XX

DT 25-MAR-2003 (updated)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Domain	49..70
----	--------	--------

FT		/label= transmembrane
----	--	-----------------------

FT	Domain	80..700
----	--------	---------

FT		/label= transmembrane
----	--	-----------------------

FT	Domain	115..136
----	--------	----------

FT		/label= transmembrane
----	--	-----------------------

FT	Domain	154..178
----	--------	----------

FT		/label= transmembrane
----	--	-----------------------

FT	Domain	204..231
----	--------	----------

FT		/label= transmembrane
----	--	-----------------------

FT	Domain	244..268
----	--------	----------

FT		/label= transmembrane
----	--	-----------------------

FT	Domain	295..313
----	--------	----------

FT		/label= transmembrane
----	--	-----------------------

FT	Region	314..360
----	--------	----------

FT		/label= carboxyl tail
----	--	-----------------------

FT	Domain	1..48
----	--------	-------

FT		/label= extracellular
----	--	-----------------------

XX

PN WO9519436-A1.

XX

PD 20-JUL-1995.

XX

PF 11-JAN-1995; 95WO-US00476.

XX

PR 13-JAN-1994; 94US-0182962.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Charo I, Coughlin S;

XX

DR WPI; 1995-263866/34.

DR N-PSDB; AAQ96298.

XX

PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.

PT for identifying antagonists and for treating diseases characterised by

PT monocytic infiltrates

XX

PS Claim 2; Fig 2; 84pp; English.

XX

CC To identify and clone new members of the chemokine receptor gene

family, degenerate oligo primers were designed corresp. to the conserved sequences R79167 in the second and R79168 in the third transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and Q96300. Amplification of cDNA derived from MM6 cells with the primers yielded a number of PCR products. One cDNA appeared to encode a novel protein. To obtain a full-length version of this clone, a MM6 cDNA library was constructed in pFROG and probed with the PCR product. A 2.1 kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA library revealed a second sequence that was identical to the 2.1 kb cDNA sequence first obtd. from the 5' UTR through the putative seventh transmembrane domain but contained a different cytoplasmic tail. The second sequence appears to represent alternative splicing of the carboxyl-terminal tail of the MCP-1R protein. The two sequences are denoted MCP-1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol. wt. of about 41,000 daltons.

(Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.2e-211;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN	60
Qy	61	MLVVLI LINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFNGAMCKLFTGLY	120
Db	61	MLVVLI LINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFNGAMCKLFTGLY	120
Qy	121	HIGYFGGIFFII LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVA VFASVP GII IFTK	180
Db	121	HIGYFGGIFFII LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVA VFASVP GII IFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFH TIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFH TIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVI LLNTFQE FFGLSNCESTS QLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVI LLNTFQE FFGLSNCESTS QLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFC KQCPVFYRETVDGV TSTNTPSTGEQEVSAGL	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFC KQCPVFYRETVDGV TSTNTPSTGEQEVSAGL	360

## RESULT 2

AAW35833

ID    AAW35833 standard; Protein; 360 AA.

XX

AC      AAW35833;

XX  
 DT 27-FEB-1998 (first entry)  
 XX  
 DE Human monocyte chemoattractant protein 1 receptor.  
 XX  
 KW Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;  
 KW inflammatory disease; viral; allergy; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP09238688-A.  
 XX  
 PD 16-SEP-1997.  
 XX  
 PF 11-MAR-1996; 96JP-0053574.  
 XX  
 PR 11-MAR-1996; 96JP-0053574.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 DR WPI; 1997-506557/47.  
 DR N-PSDB; AAT96976.  
 XX  
 PT DNA encoding human monocyte chemoattractant protein 1 receptor -  
 PT used to treat tumours and inflammatory, viral, infectious, allergic,  
 PT diabetic and central nervous system diseases  
 XX  
 PS Disclosure; Page 12-14; 15pp; Japanese.  
 XX  
 CC The present sequence represents human monocyte chemoattractant protein 1  
 CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA  
 CC are used for the prevention and treatment of tumours and inflammatory,  
 CC viral, infectious, allergic, diabetic and central nervous system  
 CC diseases.  
 XX  
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 18; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-211;  
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNI LGLVLPLLIMVICYSGILKTLRLCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNI LGLVLPLLIMVICYSGILKTLRLCRNEKKRHR	240

QY 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
 QY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

RESULT 3

AAG80108

ID AAG80108 standard; Protein; 360 AA.

XX

AC AAG80108;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2b protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX

PN WO200172830-A2.

XX

PD 04-OCT-2001.

XX

PF 02-APR-2001; 2001WO-EP03708.

XX

PR 31-MAR-2000; 2000DE-1016013.

XX

PA (IPFP-) IPF PHARM GMBH.

PA (FORS/) FORSSMANN U.

XX

PI Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX

DR WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands,  
 PT useful for detecting tumors, inflammation etc., also therapeutic use of  
 PT ligand inhibitors -

XX

PS Disclosure; Page 9; 26pp; German.

XX

CC This invention describes a novel diagnostic agent (A) comprising at least  
 CC two different ligands (I) for receptors (II) that are implicated in  
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
 CC Also inhibitors of (I) are used therapeutically against tumors (and their  
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
 CC endocrine, motor or urogenital systems or skin are affected, and bone



CC marrow diseases. The products of the invention are chemokine derivatives  
CC which have cytostatic, antiinflammatory, antiasthmatic,  
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.  
CC Chemokines act on specific tumor and inflammatory cells through a  
CC constellation of chemokine receptors (CR), which control migration and  
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
CC fragments used to illustrate the method of the invention.

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 22; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.2e-211;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
```

RESULT 4

AAU07614

ID AAU07614 standard; Protein; 360 AA.

XX

AC AAU07614;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human wild-type CCR2-64V polypeptide.

XX

KW Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;  
KW single nucleotide polymorphism; hypercholesterolaemia.

XX

OS Homo sapiens.

XX

PN WO200162796-A1.

XX

PD 30-AUG-2001.

QY 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Db 241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360

Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 5

ABP97725

ID ABP97725 standard; Protein; 360 AA.

XX

AC ABP97725;

XX

DT 28-MAY-2003 (first entry)

XX

DE Amino acid sequence of human chemokine receptor CCR2.

XX

KW Human; chemokine receptor; CCR2; viral infection; surface protein;

KW respiratory virus infection; respiratory syncytial virus infection;

KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.

XX

OS Homo sapiens.

XX

PN WO2003014153-A2.

XX

PD 20-FEB-2003.

XX

PF 12-AUG-2002; 2002WO-CA01248.

XX

PR 10-AUG-2001; 2001US-311088P.

XX

PA (TOPI-) TOPIGEN PHARM INC.

XX

PI Renzi P, Zemzoumi K, Lamkhioued B;

XX

DR WPI; 2003-247991/25.

DR N-PSDB; ABZ68878.

XX

PT Modulating viral infection of a cell, for treating or preventing  
PT respiratory virus infections, bronchitis, pneumonia or asthma, by  
PT modulating a binding interaction between a cell chemokine-receptor and  
PT a surface protein of the virus -

XX

PS Disclosure; Page 82-84; 120pp; English.

XX

CC The present sequence represents human chemokine receptor CCR2. The  
CC specification describes a method for modulating viral infection of  
CC a cell. the method comprises modulating a binding interaction between  
CC a cell chemokine-receptor and a surface protein of the virus. The  
CC proviso is that the cell chemokine-receptor is not CX3CR1 and that the  
CC virus is not HIV. The method is useful for treating or preventing  
CC respiratory virus infection in vertebrates, more particularly  
CC respiratory syncytial virus (RSV) infections, and related diseases,  
CC e.g. bronchiolitis, bronchitis, pneumonia or asthma.

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 24; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-211;  
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

```

RESULT 6

ABP81987

ID ABP81987 standard; Protein; 360 AA.

XX

AC ABP81987;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human C-C chemokine receptor 2 protein SEQ ID NO:460.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX





PS Claim 1; Page 20; 28pp; English.

XX

CC The invention relates to diagnosing atherosclerosis (or susceptibility  
CC to) in a subject by determining expression or activity of the human  
CC CCR2-64I polypeptide (a polymorphic variant form of the human CCR2  
CC receptor) or the CCR2-64V polypeptide (human CCR2 receptor), by screening  
CC for a single nucleotide polymorphism in codon 64 of the polynucleotide  
CC encoding the CCR2 receptor. This results in production of CCR2-64I,  
CC whereby polymorphic variants are associated with a lower incidence of  
CC atherosclerosis. The presence or amount of CCR2-64I/V in a sample can  
CC also be analysed. The sequences of the invention can be used for  
CC predicting the response of a patient to drug treatment, for predicting  
CC the disease outcome in a patient and also for the production of a  
CC treatment for hypercholesterolaemia. The sequence represents the  
CC polymorphic variant polypeptide CCR2-64I.

XX

SQ Sequence 360 AA;

Query Match 99.9%; Score 1899; DB 22; Length 360;  
Best Local Similarity 99.7%; Pred. No. 4.2e-211;  
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
          |||:
Db     61 MLVILILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
          |||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
```

#### RESULT 8

ABB56340

ID ABB56340 standard; Protein; 360 AA.

XX

AC ABB56340;

XX

DT 18-FEB-2002 (first entry)

XX

DE Non-endogenous human GPCR protein, SEQ ID NO: 473.

XX







DR WPI; 1995-263866/34.  
 DR N-PSDB; AAQ96297.  
 XX  
 PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
 PT for identifying antagonists and for treating diseases characterised by  
 PT monocytic infiltrates  
 XX  
 PS Claim 2; Fig 1; 84pp; English.  
 XX  
 CC To identify and clone new members of the chemokine receptor gene  
 CC family, degenerate oligo primers were designed corresp. to the  
 CC conserved sequences R79167 in the second and R79168 in the third  
 CC transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8  
 CC receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293).  
 CC The degenerate oligo incorporating EcoRI and XhoI sites at their 5'  
 CC ends are Q96299 and Q96300. Amplification of cDNA derived from MM6  
 CC cells with the primers yielded a number of PCR products. One cDNA  
 CC appeared to encode a novel protein. To obtain a full-length version  
 CC of this clone, a MM6 cDNA library was constructed in pFROG and probed  
 CC with the PCR product. A 2.1 kb cDNA clone was obtd. Analysis of  
 CC additional clones in the MM6 cDNA library revealed a second  
 CC sequence that was identical to the 2.1 kb cDNA sequence first obtd.  
 CC from the 5' UTR through the putative seventh transmembrane domain  
 CC but contained a different cytoplasmic tail. The second sequence  
 CC appears to represent alternative splicing of the carboxyl-terminal  
 CC tail of the MCP-1R protein. The two sequences are denoted MCP-1RA  
 CC and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature  
 CC MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB  
 CC has a mol. wt. of about 41,000 daltons.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 16; Length 374;  
 Best Local Similarity 95.5%; Pred. No. 2.1e-182;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNFNHFTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNFNHFTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334  
 ||||| ||| |:  
 Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 10

AAG80107

ID AAG80107 standard; Protein; 374 AA.

XX

AC AAG80107;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2a protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX

PN WO200172830-A2.

XX

PD 04-OCT-2001.

XX

PF 02-APR-2001; 2001WO-EP03708.

XX

PR 31-MAR-2000; 2000DE-1016013.

XX

PA (IPFP-) IPF PHARM GMBH.

PA (FORS/) FORSSMANN U.

XX

PI Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX

DR WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands,  
 PT useful for detecting tumors, inflammation etc., also therapeutic use of  
 PT ligand inhibitors -

XX

PS Disclosure; Page 9; 26pp; German.

XX

CC This invention describes a novel diagnostic agent (A) comprising at least  
 CC two different ligands (I) for receptors (II) that are implicated in  
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
 CC Also inhibitors of (I) are used therapeutically against tumors (and their  
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
 CC endocrine, motor or urogenital systems or skin are affected, and bone  
 CC marrow diseases. The products of the invention are chemokine derivatives  
 CC which have cytostatic, antiinflammatory, antiasthmatic,  
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.  
 CC Chemokines act on specific tumor and inflammatory cells through a

CC constellation of chemokine receptors (CR), which control migration and  
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
CC fragments used to illustrate the method of the invention.

XX

SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 22; Length 374;  
Best Local Similarity 95.5%; Pred. No. 2.1e-182;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334
      |||
Db    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
```

RESULT 11

ABG92881

ID ABG92881 standard; Peptide; 344 AA.

XX

AC ABG92881;

XX

DT 19-NOV-2002 (first entry)

XX

DE Class I receptors WSXWS motif.

XX

KW Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDG NR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX

OS Synthetic.

XX  
 PN WO200264612-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 08-FEB-2002; 2002WO-US03634.  
 XX  
 PR 09-FEB-2001; 2001US-0779880.  
 PR 09-FEB-2001; 2001WO-US04153.  
 PR 12-JUN-2001; 2001US-297257P.  
 PR 08-AUG-2001; 2001US-310458P.  
 PR 12-OCT-2001; 2001US-328447P.  
 PR 21-DEC-2001; 2001US-341725P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Roschke V, Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2002-643455/69.  
 XX  
 PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGNR10 e.g. cancer -  
 XX  
 PS Example 17; Page 386; 562pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,  
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia,  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human  
 CC G-protein chemokine receptor (CCR5) HDGNR10. This is the amino acid  
 CC sequence of the WSXWS motif found in class I receptors.  
 XX  
 SQ Sequence 344 AA;

Query Match 82.6%; Score 1568.5; DB 23; Length 344;  
 Best Local Similarity 95.3%; Pred. No. 8e-173;  
 Matches 302; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77  
 |||





Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRLYS 317  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR---S 282

Qy 318 VFFRKHITKRFCQCPV 334  
 :| || |: |:  
 Db 283 LF---HIALG-CRIAPL 295

# RESULT 13

ABB81055

ID ABB81055 standard; Protein; 329 AA.

XX

AC ABB81055;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human MCP-1 receptor.

XX

KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDG NR10;

KW G-protein chemokine receptor; haematopoietic; immunosuppressant;

KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;

KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.

XX

OS Homo sapiens.

XX

PN US2002076745-A1.

XX

PD 20-JUN-2002.

XX

PF 18-NOV-1998; 98US-0195662.

XX

PR 06-JUN-1995; 95US-0466343.

XX

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2002-598724/64.

XX

PT New polynucleotide encoding a human G protein chemokine receptor

PT HDG NR10, useful e.g. for treating tumors -

XX

PS Examples; Fig 2; 22pp; English.

XX

CC The invention relates to a novel human 7-transmembrane receptor, HDG NR10,  
 CC which has been identified as a G-protein chemokine receptor. The GPCR  
 CC HDG NR10 polypeptide can be expressed by standard recombinant methodology.  
 CC Compounds that activate or inhibit the receptor polypeptide, optionally  
 CC expressed from DNA in gene therapy vectors, are used to treat diseases  
 CC that require: (a) activation of the receptor (e.g. stimulation of  
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune  
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the  
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis  
 CC etc). The present sequence represents a human MCP-1 receptor used in



CC comparison studies with the HDGMR10 receptor.

XX

SQ Sequence 329 AA;

Query Match 77.5%; Score 1473; DB 23; Length 329;  
Best Local Similarity 90.5%; Pred. No. 8.8e-162;  
Matches 287; Conservative 3; Mismatches 5; Indels 22; Gaps 4;

```
Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLT 77
          |||
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHI----- 105

Qy     138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          |||
Db     106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWT 257
          |||
Db     166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWT 225

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRLYS 317
          |||
Db     226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR---S 282

Qy     318 VFFRKHITKRFCCKQCPV 334
          :|  ||  |: |:
Db     283 LF---HIALG-CRIAPL 295
```

#### RESULT 14

AAW54037

ID AAW54037 standard; Protein; 354 AA.

XX

AC AAW54037;

XX

DT 06-AUG-1998 (first entry)

XX

DE Mouse CC-CKR5 protein.

XX

KW CC-CKR5; chemokine receptor; mouse; human; transgenic mouse;

KW HIV infection; T-cell mediated inflammation.

XX

OS Mus sp.

XX

PN EP834564-A2.

XX

PD 08-APR-1998.

XX

PF 03-OCT-1997; 97EP-0307823.

XX

PR 03-OCT-1996; 96US-0724984.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.



DT 10-DEC-2001 (first entry)  
 XX  
 DE Amino acid sequence of human CCR5 protein.  
 XX  
 KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV;  
 KW gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;  
 KW HIV infection; CCR5.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200164752-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US06322.  
 XX  
 PR 02-MAR-2000; 2000US-0517605.  
 XX  
 PA (UYNY ) UNIV NEW YORK STATE.  
 PA (UYNI-) UNIV NIJMEGEN.  
 XX  
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;  
 XX  
 DR WPI; 2001-602565/68.  
 XX  
 PT An antibody for the treatment or prevention of HIV-infection comprises  
 PT a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding  
 PT of DC-SIGN due to concomitant conformational change -  
 XX  
 PS Disclosure; Page 118-119; 131pp; English.  
 XX  
 CC The specification describes an antibody which is specific for an  
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN  
 CC or is exposed upon gp120 binding of DC-SIGN due to concomitant  
 CC conformational change. DC-SIGN is a receptor that is specifically  
 CC expressed on dendritic cells and facilitates infection of T lymphocytes  
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.  
 CC DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)  
 CC with high affinity. The antibody of the invention inhibits the trans  
 CC enhancement of HIV entry into a T cell or macrophage facilitated by  
 CC dendritic cells. The antibody is useful to treat or prevent HIV  
 CC infection. The present sequence represents a human CCR5 protein,  
 CC which is a translocation promoting agent that interacts with CD4.  
 CC This receptor functions in HIV-1 entry into cells.  
 XX  
 SQ Sequence 352 AA;

Query Match 72.2%; Score 1371; DB 22; Length 352;  
 Best Local Similarity 76.2%; Pred. No. 6.4e-150;  
 Matches 259; Conservative 30; Mismatches 47; Indels 4; Gaps 1;

Qy 25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84  
 ||| || | :||| |:|||||:|||||:|:|||||:|:|||||  
 Db 13 DYDTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILVLINCKRLKSMTDIYLLNL 72  
 Qy 85 AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH 144  
 ||||| ||:|:| ||| || :| ||| ||:| ||||| ||:| |||||

Db 73 AISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAIVH 132  
 Qy 145 AVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RGWNN 200  
 |||||:|||||:|||||: ||| :|| : ||  
 Db 133 AVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHFYPYSQYQFWKN 192  
 Qy 201 FHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYN 260  
 | |: |||||:|||||:|||||:|||||: |||  
 Db 193 FQTLKIVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYN 252  
 Qy 261 IVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFF 320  
 ||:|||||: || |: ||| |||||:|||||: |||  
 Db 253 IVLLLNTFQEFFGLNNCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312  
 Qy 321 RKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360  
 :||| | ||| | :| :| : :| | |||||: |||  
 Db 313 QKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352

Search completed: November 25, 2003, 23:19:10  
 Job time : 46 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 23:20:40 ; Search time 31 Seconds  
(without alignments)  
2141.922 Million cell updates/sec

Title: US-09-625-573-4  
Perfect score: 1900  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTTSTNTPSTGEQEVSAAGL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	1900	100.0	360	9	US-09-131-827A-2	Sequence 2, Appli
2	1900	100.0	360	12	US-10-164-649-50	Sequence 50, Appl
3	1900	100.0	360	12	US-10-239-423-64	Sequence 64, Appl
4	1900	100.0	360	12	US-10-439-845-8	Sequence 8, Appli
5	1900	100.0	360	15	US-10-225-567A-460	Sequence 460, App
6	1899	99.9	360	9	US-09-131-827A-20	Sequence 20, Appl
7	1894	99.7	360	12	US-09-826-509-473	Sequence 473, App
8	1873	98.6	360	10	US-09-938-719-7	Sequence 7, Appli
9	1873	98.6	360	10	US-09-939-226-7	Sequence 7, Appli
10	1873	98.6	360	10	US-09-938-703-7	Sequence 7, Appli
11	1849	97.3	360	12	US-10-164-649-51	Sequence 51, Appl
12	1838	96.7	347	9	US-09-104-792-3	Sequence 3, Appli
13	1838	96.7	347	12	US-10-176-078-3	Sequence 3, Appli
14	1651.5	86.9	374	12	US-10-239-423-63	Sequence 63, Appl
15	1568.5	82.6	344	9	US-09-779-879A-9	Sequence 9, Appli
16	1568.5	82.6	344	9	US-09-779-880A-9	Sequence 9, Appli
17	1568.5	82.6	344	12	US-10-135-839-9	Sequence 9, Appli
18	1568.5	82.6	344	15	US-10-232-686-9	Sequence 9, Appli
19	1568.5	82.6	344	15	US-10-067-800-9	Sequence 9, Appli
20	1473	77.5	329	9	US-09-725-285-9	Sequence 9, Appli
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23	1473	77.5	329	10	US-09-502-783A-9	Sequence 9, Appli
24	1370	72.1	352	12	US-10-164-649-52	Sequence 52, Appl
25	1364	71.8	352	9	US-09-759-841-2	Sequence 2, Appli
26	1364	71.8	352	9	US-09-813-653-15	Sequence 15, Appl
27	1364	71.8	352	9	US-09-796-202-1	Sequence 1, Appli
28	1364	71.8	352	10	US-09-938-719-5	Sequence 5, Appli
29	1364	71.8	352	10	US-09-939-226-5	Sequence 5, Appli
30	1364	71.8	352	10	US-09-938-703-5	Sequence 5, Appli
31	1364	71.8	352	11	US-09-734-221A-14	Sequence 14, Appl
32	1364	71.8	352	12	US-10-323-314-1	Sequence 1, Appli
33	1364	71.8	352	12	US-10-072-301-1	Sequence 1, Appli
34	1364	71.8	352	12	US-10-071-866-1	Sequence 1, Appli
35	1364	71.8	352	12	US-10-239-423-67	Sequence 67, Appl
36	1364	71.8	352	12	US-10-439-845-4	Sequence 4, Appli
37	1364	71.8	352	12	US-10-360-828-1	Sequence 1, Appli
38	1364	71.8	352	14	US-10-106-623-2	Sequence 2, Appli
39	1364	71.8	352	14	US-10-106-623-20	Sequence 20, Appl
40	1364	71.8	352	15	US-10-086-814-1	Sequence 1, Appli
41	1364	71.8	352	15	US-10-290-058A-6	Sequence 6, Appli
42	1364	71.8	352	15	US-10-225-567A-352	Sequence 352, App
43	1359	71.5	352	12	US-10-439-845-2	Sequence 2, Appli
44	1358	71.5	352	9	US-09-813-653-17	Sequence 17, Appl
45	1358	71.5	352	12	US-09-826-509-477	Sequence 477, App

#### ALIGNMENTS

RESULT 1  
 US-09-131-827A-2  
 ; Sequence 2, Application US/09131827A  
 ; Patent No. US20020038469A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dean, Michael

```
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2
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Best Local Similarity 100.0%; Pred. No. 1.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
```

## RESULT 2

US-10-164-649-50

; Sequence 50, Application US/10164649

; Publication No. US20030162943A1

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

```

;      ADDRESSEE: LAHIVE & COCKFIELD, LLP
;      STREET: 28 State Street
;      CITY: Boston
;      STATE: Massachusetts
;      COUNTRY: USA
;      ZIP: 02109
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/164,649
;      FILING DATE: 07-Jun-2002
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/045,583
;      FILING DATE: 20-MAR-1998
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Mandragouras, Amy E.
;      REGISTRATION NUMBER: 36,207
;      REFERENCE/DOCKET NUMBER: MNI-044
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (617)227-7400
;      TELEFAX: (617)742-4214
;
;      INFORMATION FOR SEQ ID NO: 50:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 360 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FRAGMENT TYPE: internal
;      SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-164-649-50

```

```

Query Match          100.0%;  Score 1900;  DB 12;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 1.5e-150;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||

```



```

Db      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
        |||
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

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RESULT 3

US-10-239-423-64

```

; Sequence 64, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells
and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand
Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-64

```

```

Query Match          100.0%; Score 1900; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Qy      61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
        |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
        |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

```

```

QY      241 AVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

QY      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360

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RESULT 4

US-10-439-845-8

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; Sequence 8, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
;   APPLICANT:  Combadiere et al.,
;   TITLE OF INVENTION:  CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
;   TITLE OF INVENTION:  AND THERAPEUTIC AGENTS FOR HIV INFECTION
;   NUMBER OF SEQUENCES:  9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Fish & Richardson P.C.
;     STREET:  4225 Executive Square, Suite 1400
;     CITY:  La Jolla
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/10/439,845
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/864,458
;     FILING DATE:  May 28, 1997
;     APPLICATION NUMBER:  Provisional 60/018,508
;     FILING DATE:  May 28, 1996
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Haile, Lisa A.
;     REGISTRATION NUMBER:  38,347
;     REFERENCE/DOCKET NUMBER:  08830/030001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  619/678-5070
;     TELEFAX:  619/678-5099
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  360 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-10-439-845-8

```

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Query Match          100.0%;  Score 1900;  DB 12;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 1.5e-150;

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Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Qy          61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
            |||:|||||
Db          61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
Qy          121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
            |||:|||||
Db          121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Qy          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
            |||:|||||
Db          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
Qy          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
            |||:|||||
Db          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy          301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
            |||:|||||
Db          301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

```

# RESULT 6

US-09-131-827A-20

```

; Sequence 20, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

```

```

Query Match          99.9%; Score 1899; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.8e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
            |||:|||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Qy          61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
            |||:|||||

```

```

Db          61 MLVILILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
Qy          121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db          121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Qy          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db          181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
Qy          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQE FFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||
Db          241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQE FFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy          301 NPIIYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
          |||
Db          301 NPIIYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

```

# RESULT 7

```

US-09-826-509-473
; Sequence 473, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-473

```

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Query Match          99.7%; Score 1894; DB 12; Length 360;
Best Local Similarity 99.7%; Pred. No. 4.7e-150;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDY GAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
          |||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDY GAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
Qy          61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          |||
Db          61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

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; TOPOLOGY: linear  
; MOLECULE TYPE: No. US20020106742A1e  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-938-719-7

Query Match 98.6%; Score 1873; DB 10; Length 360;  
Best Local Similarity 98.3%; Pred. No. 2.7e-148;  
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
          ||||||||||||||||||||||||||||:||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPPLLIMVICYSGILKTLLRCRNEKKRHR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQAIQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
          ||||||||||||||||:||||||| ||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
```

RESULT 9  
US-09-939-226-7  
; Sequence 7, Application US/09939226  
; Patent No. US20020110805A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;      SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/939,226
;      FILING DATE: 24-Aug-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 09/626,939
;      FILING DATE: 2000-07-27
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Altman, Daniel E
;      REGISTRATION NUMBER: 34,115
;      REFERENCE/DOCKET NUMBER: <Unknown>
;
;      INFORMATION FOR SEQ ID NO: 7:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 360 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: No. US20020110805A1e
;      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-939-226-7

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Query Match          98.6%;  Score 1873;  DB 10;  Length 360;
Best Local Similarity 98.3%;  Pred. No. 2.7e-148;
Matches 354;  Conservative 2;  Mismatches 4;  Indels 0;  Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Qy     61 MLVVLILINCKKCLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db     61 MLVVLILINCKKCLKCLTDIYLLNLAI SDLLFIITLPLWAHSAANEVVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWN NFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWN NFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db    241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQAIQVTETLGMTHCCI 300

Qy    301 NP I IYAFVGEKFR RYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
        ||||||||||||||||:|||||||
Db    301 NP I IYAFVGEKFR RYISVFFRKHIXX FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

```

```

RESULT 10
US-09-938-703-7
; Sequence 7, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL

```





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Db      181 CQKEDSVYVCGPYFPRGWNFHTIMRNI LGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
QY      241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      |||||||
Db      241 AVRVI FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQAIQVTETLGMTHCCI 300
QY      301 NP IIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      |||||||: |||||
Db      301 NP IIYAFVGEKFRRYISVFFRKHIXXFXCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

```

RESULT 11

US-10-164-649-51

; Sequence 51, Application US/10164649

; Publication No. US20030162943A1

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. US20030162943A1e1 Molecules of the G Protein-

Coupled

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/164,649

; FILING DATE: 07-Jun-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/045,583

; FILING DATE: 20-MAR-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: MNI-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 51:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-10-164-649-51

Query Match

97.3%; Score 1849; DB 12; Length 360;

Best Local Similarity 97.2%; Pred. No. 2.7e-146;  
Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
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Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Db    121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNI LGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      ||:|||||:|||||
Db    181 CQEEDSVYICGPYFPRGWNNFHTIMRNI LGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNI VILLNTFQE FFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      |||:|||||
Db    241 AVRLIPTIMIVYFLFWTPYNI VILLNTFQE FFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
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Db    301 NPIIYAFVGEKFRRYLSMFFRKYITKR FCKQCPVFYRETVDGVTSTNTPSTAEQEV SAGL 360
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RESULT 12

US-09-104-792-3

; Sequence 3, Application US/09104792

; Patent No. US20020019026A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Yi, Li

; APPLICANT: Ruben, Steven M.

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,792

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-104-792-3

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Query Match          96.7%; Score 1838; DB 9; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.1e-145;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      14 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKL 73
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKL 60

Qy      74 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 133
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 120

Qy     134 LTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY 193
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY 180

Qy     194 FPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIIFTIMIVYF 253
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIIFTIMIVYF 240

Qy     254 LFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFR 300

Qy     314 RYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSA GL 360
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Db     301 RYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSA GL 347

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RESULT 13

US-10-176-078-3

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; Sequence 3, Application US/10176078
; Publication No. US20030165901A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
;           Yi, Li
;           Ruben, Steven M.
;           Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

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Db      241 LFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 300

Qy      314 RYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
          |||
Db      301 RYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 347

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RESULT 14

US-10-239-423-63

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; Sequence 63, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells
and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand
Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-63

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Query Match      86.9%; Score 1651.5; DB 12; Length 374;
Best Local Similarity 95.5%; Pred. No. 8.1e-130;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
          |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLPLLMVICYSGILKTLRLCRNEKKRHR 240
          |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLPLLMVICYSGILKTLRLCRNEKKRHR 240

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Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
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 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334  
 ||| :| || |: |  
 Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 15

US-09-779-879A-9  
 ; Sequence 9, Application US/09779879A  
 ; Patent No. US20020048786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, Craig A.  
 ; APPLICANT: Roschke, Viktor  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10  
 ; FILE REFERENCE: 1488.115000A  
 ; CURRENT APPLICATION NUMBER: US/09/779,879A  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/181,258  
 ; PRIOR FILING DATE: 2000-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/187,999  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: US 60/234,336  
 ; PRIOR FILING DATE: 2000-09-22  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-779-879A-9

Query Match 82.6%; Score 1568.5; DB 9; Length 344;  
 Best Local Similarity 95.3%; Pred. No. 6.1e-123;  
 Matches 302; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLT 77  
 |||  
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137  
 |||  
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy 138 RYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197  
 |||  
 Db 121 RYLAIHVAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy 198 WNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHRVAVRVIPTIMIVYFLFWT 257  
 |||  
 Db 181 WNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHRVAVRVIPTIMIVYFLFWT 240

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317

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      |||||
Db      241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR---S 297
      |||||
Qy      318 VFFRKHITKRFCQCPV 334
      :|  ||  |: |:
Db      298 LF---HIALG-CRIAPL 310

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Search completed: November 25, 2003, 23:26:06  
Job time : 32 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 23:16:34 ; Search time 20 Seconds  
(without alignments)  
1731.036 Million cell updates/sec

Title: US-09-625-573-4  
Perfect score: 1900  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNPSTGEQEVSAAGL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1900	100.0	360	2	JC2443	chemokine (C-C) re
2	1651.5	86.9	374	2	I38450	chemokine (C-C) re
3	1364	71.8	352	2	A43113	chemokine (C-C) re
4	1036	54.5	355	2	A45177	chemokine (C-C) re
5	1010.5	53.2	359	2	I49341	MIP-1 alpha recept
6	963.5	50.7	355	2	I49339	macrophage inflamm
7	951	50.1	355	2	G02436	chemokine (C-C) re
8	871	45.8	360	2	JC4587	chemokine (C-C) re
9	862.5	45.4	360	2	A57160	chemokine (C-C) re
10	822.5	43.3	383	2	S55594	G protein-coupled
11	778.5	41.0	356	2	I49340	MIP-1 alpha recept
12	751	39.5	355	2	JC5067	G protein-coupled
13	722.5	38.0	354	2	I58186	probable G protein

14	708	37.3	355	2	JC4304	orphan G protein-c
15	649.5	34.2	344	2	JC5942	chemokine receptor
16	581.5	30.6	378	2	B55735	lymphocyte-specifi
17	569	29.9	378	2	A55735	G protein-coupled
18	567.5	29.9	378	2	A45680	G protein-coupled
19	563	29.6	369	2	JC5068	G protein-coupled
20	547	28.8	360	2	A53611	interleukin-8 rece
21	540.5	28.4	355	2	JQ1231	interleukin-8 rece
22	540.5	28.4	359	2	A48921	interleukin-8 rece
23	536.5	28.2	358	2	A53752	interleukin-8 rece
24	532.5	28.0	356	2	S42096	interleukin-8 rece
25	532	28.0	367	2	JE0349	interferon-inducib
26	528.5	27.8	333	2	I65989	G protein-coupled
27	528.5	27.8	350	2	A39445	interleukin-8 rece
28	515.5	27.1	352	2	G00048	fusin (LESTRA) - c
29	515	27.1	353	2	S28787	neuropeptide Y/pep
30	512.5	27.0	352	2	A45747	neuropeptide Y/pep
31	495.5	26.1	350	2	JN0621	G protein-coupled
32	486.5	25.6	359	2	S15403	angiotensin II rec
33	480.5	25.3	359	2	A42656	angiotensin II rec
34	480	25.3	374	2	S42628	G protein-coupled
35	475.5	25.0	359	2	JC2134	angiotensin II rec
36	474.5	25.0	359	2	JC1104	angiotensin II rec
37	474.5	25.0	359	2	S44425	angiotensin II rec
38	472.5	24.9	359	2	JH0621	angiotensin II rec
39	471.5	24.8	359	2	JQ1516	angiotensin II rec
40	469.5	24.7	359	2	JC1194	angiotensin II rec
41	468.5	24.7	359	2	I51372	angiotensin II rec
42	466	24.5	359	2	A48857	angiotensin II rec
43	465.5	24.5	374	2	S32785	G protein-coupled
44	465	24.5	327	2	S56162	MDCR15 protein - h
45	465	24.5	372	2	S26667	G protein-coupled

#### ALIGNMENTS

##### RESULT 1

JC2443

chemokine (C-C) receptor 2, splice form B - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor;

monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 20-Jun-2000

C;Accession: JC2443; I38463

R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.

Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994

A;Title: cDNA cloning and functional expression of a human monocyte  
chemoattractant protein 1 receptor.

A;Reference number: JC2443; MUID:94324942; PMID:8048929

A;Accession: JC2443

A;Molecule type: mRNA

A;Residues: 1-360 <YAM>

A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247

R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin,  
S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-360 <RES>

A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;43-70/Domain: transmembrane #status predicted <TM1>

F;81-100/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;207-226/Domain: transmembrane #status predicted <TM5>

F;244-268/Domain: transmembrane #status predicted <TM6>

F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1900; DB 2; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.9e-154;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60

Qy     61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
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Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

Qy    241 AVRVIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRVIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NP I IYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      |||
Db    301 NP I IYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
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RESULT 2

I38450

chemokine (C-C) receptor 2, splice form A - human  
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor;  
monocyte chemotactin 1 receptor  
C;Species: Homo sapiens (man)  
C;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
C;Accession: I38450  
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin,  
S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A;Title: Molecular cloning and functional expression of two monocyte  
chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-  
terminal tails.  
A;Reference number: A53477; MUID:94195821; PMID:8146186  
A;Accession: I38450  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <RES>  
A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556  
C;Genetics:  
A;Gene: GDB:CMKBR2  
A;Cross-references: GDB:337364; OMIM:601267  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein;  
transmembrane protein  
F;44-68/Domain: transmembrane #status predicted <TM1>  
F;79-99/Domain: transmembrane #status predicted <TM2>  
F;115-136/Domain: transmembrane #status predicted <TM3>  
F;154-178/Domain: transmembrane #status predicted <TM4>  
F;208-226/Domain: transmembrane #status predicted <TM5>  
F;244-265/Domain: transmembrane #status predicted <TM6>  
F;292-309/Domain: transmembrane #status predicted <TM7>  
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 86.9%; Score 1651.5; DB 2; Length 374;  
Best Local Similarity 95.5%; Pred. No. 5.5e-133;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLPPLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLPPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||

```

Db 241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSOLDOATOVTTETLGMTHCCI 300

Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

### RESULT 3

A43113

chemokine (C-C) receptor 5 - human

N;Alternate names: C-C CKR-5; CCR5

C; Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000

C;Accession: A43113; S71808; A58834; A58832; G02653; A58833

R; Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor gene.

A;Reference number: A43113; MUID:96241590; PMID:8639485

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A; Cross-references: GB:X91492; NID:q1262810; PIDN:CAA62796.1; PID:q1262811

R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.;

Saragosti, S.; Lapoumeroulie, C.; Cognaux, J.; Forceille, C.; Muyldermans, G.;

Verhofstede, C.; Burtonboy, G.; Georges, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth,

R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene.

A;Reference number: S71808; MUID:96345670; PMID:8751444

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184, 'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <SAM3>

A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A; Note: this frameshift mutation results in a non-functional receptor but

confers a degree of resistance to HIV-1 infection; it has an allele frequency of 0.09 or more in some caucasian populations and may have had a selective advantage by conferring resistance to Yersinia plague infections

R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1alpha, MIP-1beta, and RANTES.

A;Reference number: A58832; MUID:96295970; PMID:8699119

A;Accession: A58832

A;Molecule type: mRNA

A;Residues: 1-352 <COM1>

A;Cross-references: GB:U57840; NID:q1502408; PIDN:AAB17071.1; PID:q1502409

A; Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R; Combadiere, C.

submitted to the EMBL Data Library, May 1996

A;Reference number: H01541

A;Accession: G02653

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-89,'L',91-352 <COM2>

A;Cross-references: EMBL:U57840

R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996

A;Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.

A;Reference number: A58833; MUID:96291862; PMID:8663314

A;Accession: A58833

A;Molecule type: mRNA

A;Residues: 1-352 <RAP>

A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946

C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A31767), and RANTES (see PIR:A28815).

C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 5 and T-cell surface glycoprotein CD4 (see PIR:RWHUT4).

C;Genetics:

A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13

A;Cross-references: GDB:1230510; OMIM:601373

A;Map position: 3p21-3p21

C;Function:

A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES

A;Note: probably acts to control granulocyte proliferation and differentiation

C;Superfamily: vertebrate rhodopsin

C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;32-56/Domain: transmembrane #status predicted <TM1>

F;67-87/Domain: transmembrane #status predicted <TM2>

F;103-124/Domain: transmembrane #status predicted <TM3>

F;142-166/Domain: transmembrane #status predicted <TM4>

F;193-218/Domain: transmembrane #status predicted <TM5>

F;236-257/Domain: transmembrane #status predicted <TM6>

F;285-300/Domain: transmembrane #status predicted <TM7>

F;20-269,101-178/Disulfide bonds: #status predicted

F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted

F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 71.8%; Score 1364; DB 2; Length 352;

Best Local Similarity 75.5%; Pred. No. 1.5e-108;

Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

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Qy      24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| :|      || | :||| |:|||||:|||||:|||||:|||||:|||||:|||||
Db      10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69

Qy      82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      ||||| ||:|:| ||| || :| ||| ||:| |||| ||:| |||||:|||||
Db      70 LNLAISDLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy     142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

Db      130 VVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHPYSQYQF 189
Qy      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
      | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      190 WKNFQTLKIVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 249
Qy      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      250 PYNIVLLLNTFQEFFGLNNCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
Qy      318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGGEQEVSAAGL 360
      | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGGEQEISVGL 352

```

#### RESULT 4

A45177

chemokine (C-C) receptor 1 - human

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999

C;Accession: A45177; I55671

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Accession: A45177

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-355 <NEO>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A;Experimental source: HL60 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Accession: I55671

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-355 <RES>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C;Genetics:

A;Gene: GDB:CMKBR1; CMKR-1

A;Cross-references: GDB:138446; OMIM:601159

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;36-60/Domain: transmembrane #status predicted <TM1>

F;71-91/Domain: transmembrane #status predicted <TM2>

F;108-129/Domain: transmembrane #status predicted <TM3>

F;147-171/Domain: transmembrane #status predicted <TM4>

F;205-223/Domain: transmembrane #status predicted <TM5>

F;240-264/Domain: transmembrane #status predicted <TM6>

F;288-305/Domain: transmembrane #status predicted <TM7>  
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;24-273,106-183/Disulfide bonds: #status predicted  
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 54.5%; Score 1036; DB 2; Length 355;  
Best Local Similarity 56.4%; Pred. No. 1.2e-80;  
Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

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Qy      12 NTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK 71
      ||| | : || ||| || | : : ||||| ||||| : | |||: |||: | : |
Db      5 NTTED-YDTTTEFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYK 63

Qy      72 KLKCLTDIYLLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIF 130
      : || : | ||||| ||||| || | : : ||||| ||||| : | | : | : |||
Db      64 RLKNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYTGlySEIFF 123

Qy     131 IILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVC 190
      ||||| ||||| ||||| ||||| : ||||| ||||| : ||| | : | : | : |
Db     124 IILLTIDRYLAIVHAVFALRARTVTFGVITSIIWALAILASMPGLYFSKTQWEFTHHTC 183

Qy     191 GPYFP---RGWNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHRVAVRVIF 246
      : || | | | : | : ||||| ||||| : ||||| |||| | ||| : ||| : ||
Db     184 SLHFPHESLREWKLQALKLNLFGLVLPPLVMIICYTGIIKILLRRPNEKK-SKAVRLIF 242

Qy     247 TIMIVYFLFWTPYNIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYA 306
      ||| : ||||| ||||| : || : || : || : || : || : || : || : ||
Db     243 VIMIIFFLFWTPYNLTILISVFQDFLFTHCEQSRHLDLAVQVTEVIAYTHCCVNPVIYA 302

Qy     307 FVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSA 359
      ||||| : ||| | : : | | : : ||| : |||| | : |||
Db     303 FVGERFRKYLRQLFHRRVAVHLVKWLPFLSVDRLERVSST-SPSTGEHELSAG 354
```

#### RESULT 5

I49341

MIP-1 alpha receptor like-2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1998

C;Accession: I49341

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49341

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-359 <RES>

A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552

C;Superfamily: vertebrate rhodopsin

Query Match 53.2%; Score 1010.5; DB 2; Length 359;  
Best Local Similarity 53.5%; Pred. No. 1.8e-78;  
Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;



Qy	10	IRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIIGFVGNMLVVLILIN	69
Db	8	IKTVVESFE--TTPYEYEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIK	65
Qy	70	CKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI	128
Db	66	YRKLQIMTNIYLFNLAISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYYLALYSEI	125
Qy	129	FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY	188
Db	126	FFIILLTIDRYLAIVHAVFALRARTVTFATITSII TWGLAGLAALPEFIFHESQDSFGEF	185
Qy	189	VCGPYFPRG---WNNFHTIMRNI LGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRV	244
Db	186	SCSPRYPEGEEDSWKRFHALRMNIFGLALPLLVMVICYSGIIKTLLRCPN-KKKHKAIRL	244
Qy	245	IFTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPII	304
Db	245	IFVVMIVFFIFWTPYNLVLLFSAPFHSTFLETSCESQSKHLDLMAQVTEVIAYTHCCVNPVI	304
Qy	305	YAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETV-----DGVSTSTNPSTGSEQEV	356
Db	305	YAFVGERFRKHLRLFFHRNVQ-----FTWENIFQFLPGEENGRTSSVSPSTGQEIEI	355
Qy	357	S 357	
Db	356	S 356	

T49339

C;Species: Mus musculus (house mouse)

C;Accession: I49339

J. Biol. Chem. 270, 17494-17501, 1995

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <RES>

A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548

C;Superfamily: vertebrate rhodopsin

Query Match 50.7%; Score 963.5; DB 2; Length 355;  
Best Local Similarity 52.3%; Pred. No. 1.8e-74;  
Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;

Qy 81 LLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY 139  
 | |||:||||:| ||| | : :||:||||:| |||:| : ||||| |||||  
 Db 73 LFNLAUSDVFLFTLPFWIDYKLDKDDWIFGDAMCKLLSGFYLLGLYSEIFFIILLTIDRY 132

Qy 140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---- 195  
 ||||| ||||:|||| |::||:||||:|: ||:| : ||| | : | ||:|  
 Db 133 LAIVHAVFALRARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSL 192

Qy 196 RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRRAVRVIFTIMIVYFLF 255  
 : | | : |::||:||||:|:||||:|: ||| | :|: :|||:| | :::||  
 Db 193 KQWKRFQALKLNLLGLLPLLMVICYAGIIRILLR-RPSEKKVKAVRLIFAITLLFFLL 251

Qy 256 WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRY 315  
 |||||: : : ||: : ||: ||| | ||||:| ||||| ||||:| :|  
 Db 252 WTPYNLSVFSVAFQDVLFTNQCEQSKHLDLQMVTETVIAYTHCCVNPPIIYVFGVGERFWKY 311

Qy 316 LSVFFRKHITKRFCQCPVFYRETVDGV--TSTNTPSTGEQEVSA 359  
 | :||: | | :||: ||: :||| | :|||  
 Db 312 LRQLFQRHVAIPLAKWLPFL---SVDQLERTSSISPSTGEHEL 354

# RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CKR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000

C;Accession: G02436; A57237

R;Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056; PMID:7622448

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1, differs from the published sequence in having 281-Leu

C;Genetics:

A;Gene: GDB:CMKBR3

A;Cross-references: GDB:579624; OMIM:601268

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;36-60/Domain: transmembrane #status predicted <TM1>

F;71-91/Domain: transmembrane #status predicted <TM2>

F;108-129/Domain: transmembrane #status predicted <TM3>  
 F;147-171/Domain: transmembrane #status predicted <TM4>  
 F;205-223/Domain: transmembrane #status predicted <TM5>  
 F;240-261/Domain: transmembrane #status predicted <TM6>  
 F;288-305/Domain: transmembrane #status predicted <TM7>  
 F;24-273,106-183/Disulfide bonds: #status predicted  
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 50.1%; Score 951; DB 2; Length 355;  
 Best Local Similarity 52.6%; Pred. No. 2e-73;  
 Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;

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Qy      21  TTFDYDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY  80
      |::| | | | | : : | | :| | | | | | | | :| | :| | | | :| | :| | |
Db      14  TSYD-DVGLLCEKADTRALMAQFVPLYSLVFTVGLLGNNVVVMILIKYRRRLRIMTNIY  72

Qy      81  LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY  139
      || | | | | | | | | :| | | | | : | | | | : | | | | : | | | | | | | |
Db      73  LLNLAISDLLFLVTLPFWIHYVRGHNNVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY  132

Qy     140  LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR---  196
      || | | | | | | | :| | | | | :| | :| | :| | :| | :| | :| | :| |
Db     133  LAIVHAVFALRARTVTFGVITSIVTGLAVLAALPEFIFYETEELFEETLCSALYPEDTV  192

Qy     197  -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLF  255
      | :| | : | | | | | :| | | | :| | | | :| | | | :| | | | :| | | |
Db     193  YSWRHFHTRLMTIFCLVLP LLVMAICYTGI IKTLLRCPS-KKKYKAIRLIFVIMAVFFIF  251

Qy     256  WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRY  315
      || | | : || | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db     252  WTPYNVAILLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKY  311

Qy     316  LSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEV  357
      | | :| : | | :| :| | :| | :| | :| | :| | :| |
Db     312  LRHFFHRHLLMHLGRYIPFLPSEKLER-TSSVSPSTAEP  352
  
```

# RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A. Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.

A;Reference number: JC4587; MUID:96136324; PMID:8573157

A;Accession: JC4587

A;Molecule type: mRNA

A;Residues: 1-360 <HOO>

A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852

A;Experimental source: thymus

C;Genetics:

A;Gene: cc ckr-4

C;Superfamily: vertebrate rhodopsin

C;Keywords: glycoprotein; phosphoprotein; receptor; thymus  
 F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.8%; Score 871; DB 2; Length 360;  
 Best Local Similarity 47.5%; Pred. No. 1.3e-66;  
 Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;

```

Qy      10 IRNTNESGEEVTTFFDYD-YGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGNMLVVLILI 68
      : : | :      : : | :      | | | : | | | | | | | : | | | : | | : |
Db      6  VTDTTQDETVYNSYYFYESMPKPCTKEG1KAFGEVFLPPLYSLVFL LGLFGNSVVVLVLF 65

Qy      69 NCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGI 128
      | : | | : | | : | | | | | | | | | | : | | : | | : | | : | : | : |
Db      66 KYKRLKSMTDVYLLNLAI SDLLFVLSLPFWGYAADQWVFG LGLCKIVSWMYLVGFYSGI 125

Qy     129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGI IFTKCQKEDSVY 188
      | | | : | : | | | | | | | | | | : | | : | | : | | | | | : | | :
Db     126 FFIMLSIDRYLAIVHAVFSLKARTLT YGVITSLITWSVAVFASLPGLLFSTCYTEHNHT 185

Qy     189 VCGPYF---PRGWNNFHTIMRNI LGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVI 245
      | : : : | : : : | : | | : | | | : | | : | | : | | : | | : |
Db     186 YCKTQYSVNSTTWKVLSSLEINVLGLLI PLGIMLFWYSMI IRTLQHKNEKK-NRAVRMI 244

Qy     246 FTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIY 305
      | : : : : | | | | | : | : | | : | : | | | | | | | | | : | : |
Db     245 FGVVVLFLGFWTPYNVVL FLET LVELEVLQDCTLERYLDYAIQATETLGF IHCCLNPVIY 304

Qy     306 AFVGEKFRRYLSVFFRKHITKR----FCKQCPVFYRETVDGVTSTNTPSTGEQE 355
      | : | | | : | : | | | | | | | | | : | : | : | | : :
Db     305 FPLGEKFRKYITQLFR---TCRGPLVLCKHCDFLQVYSADMSSSSSYTQSTVDHD 355

```

# RESULT 9

A57160

chemokine (C-C) receptor 4 - human

N;Alternate names: C-C CKR-4

C;Species: Homo sapiens (man)

C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000

C;Accession: A57160

R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.

J. Biol. Chem. 270, 19495-19500, 1995

A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.

A;Reference number: A57160; MUID:95370289; PMID:7642634

A;Accession: A57160

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-360 <POW>

A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452

A;Note: source clone K5-5

C;Genetics:  
A;Gene: GDB:CMKBR4  
A;Cross-references: GDB:677463  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F;40-65/Domain: transmembrane #status predicted <TM1>  
F;76-97/Domain: transmembrane #status predicted <TM2>  
F;112-133/Domain: transmembrane #status predicted <TM3>  
F;151-175/Domain: transmembrane #status predicted <TM4>  
F;208-226/Domain: transmembrane #status predicted <TM5>  
F;243-264/Domain: transmembrane #status predicted <TM6>  
F;291-308/Domain: transmembrane #status predicted <TM7>  
F;29-276,110-187/Disulfide bonds: #status predicted  
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.4%; Score 862.5; DB 2; Length 360;  
Best Local Similarity 48.7%; Pred. No. 6.9e-66;  
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

```

Qy      31 PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL 90
      || | :| | |||||:| | :|| :|||:| | :|: :|:| ||||| |||||
Db      28 PCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLL 87

Qy      91 FLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALK 150
      |: :|| | : ||::||| | :||: : :| :||: ||||:|:|:| |||||:|:|:|
Db      88 FVFSLPFWGYAADQWVFGGLGLCKMISWMYLVGFYSGIFFVMLMSIDRYLAIVHAVFSLR 147

Qy     151 ARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---WNNFHTIMRN 207
      |||:|:|:|:|: || |||||:| | :|: | | : | : | :|
Db     148 ARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTKYSLNSTWKVLSSLEIN 207

Qy     208 ILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRVVRVIFTIMIVYFLFWTPYNIVILLNT 267
      |||||:| | ||: || |::|| | :||| | :|||:| | :|:|:| | :|:|:| | |
Db     208 ILGLVPLGIMLFCYSMIIRTLQHCKNEKK-NKAVKMIFAVVVLFLGFWTPYNIVLFLFET 266

Qy     268 FQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKR 327
      | | | :| | | | ||| | ||:| ||| | :|||:|:| | : | | |
Db     267 LVELEVLQDCTFERLYDAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLFK---TCR 323

Qy     328 ----FCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      |: | : : | :|: | || : : |
Db     324 GLFVLCQYCGLLQIYSADTPSSSYTQSTMDHDLHDAL 360

```

RESULT 10  
S55594

G protein-coupled receptor E1 - equine herpesvirus 2  
C;Species: equine herpesvirus 2  
C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999

C;Accession: S55594  
 R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
 J. Mol. Biol. 249, 520-528, 1995  
 A;Title: The DNA sequence of equine herpesvirus 2.  
 A;Reference number: S55594; MUID:95302501; PMID:7783207  
 A;Accession: S55594  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 1-383 <TEL>  
 A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;  
 Best Local Similarity 47.9%; Pred. No. 1.9e-62;  
 Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

```

Qy      4 TSRSRFIRNTNESGEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNM 61
      | : : : : | | : | | | | : | : | | | | : | : |
Db      32 TTIASLVPSTNSSEDDYDDLDVDYEESAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNI 91

Qy      62 LVLILINCKKLCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119
      | | | : | | : | | : | | | | | | | : | | | : | | : |
Db      92 LVVIIVIRYMKIKNLTNMLLLNLAISDLLFLTLPLFWMHYIGMYHDWTFGISLCKLLRGV 151

Qy     120 YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFT 179
      : : : : | | | | : | | | : | | : | | | : | | : |
Db     152 CYMSLYSQVFCIILLTVDRYLAVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFFH 211

Qy     180 KCQKEDSVYVCGPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNE 235
      | : : | | : | | : | : | : | | | : | | : | | |
Db     212 GHQDDNGRVQCDPYYPEMSTNVWRRRAHVAKVIMLSLILPLLIMAVCYVVIIRRLLR-RPS 270

Qy     236 KKRHRAVRVIFTIMIVYFLWTPYNIIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGM 295
      | | : : | : | | | : | | | | | | : | | : | | : |
Db     271 KKKYKAIRLIFVIMVAYFVFWTPYNIIVLLSTFHATLLNLQCALSSNLDMALLITKTVA 330

Qy     296 THCCINPIIYAFVGEKFRRLYSVFFRKHITKRFCQCP 333
      | | | | : | | | | | | : | | : : | | |
Db     331 THCCINPVIYAFVGEKFRRLHYHFFHTYVAIYLCKYIP 368

```

# RESULT 11

I49340  
 MIP-1 alpha receptor like-1 - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
 C;Accession: I49340  
 R;Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.  
 A;Reference number: I49339; MUID:95340546; PMID:7542241  
 A;Accession: I49340  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA

A;Residues: 1-356 <RES>

A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550

C;Superfamily: vertebrate rhodopsin

Query Match 41.0%; Score 778.5; DB 2; Length 356;  
Best Local Similarity 45.2%; Pred. No. 9.6e-59;  
Matches 154; Conservative 62; Mismatches 118; Indels 7; Gaps 4;

```
Qy      25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84
      | : | | : | : | | | | | | | : | : | | | : | | : | | | |
Db      18 DFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNL 77

Qy      85 AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
      | | | | : | | | | : : | : | | | | | : | | : | : | | | | | : |
Db      78 AISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYILGLYSDMFFITLLTIDRYLAVV 137

Qy     144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
      | | | | : | | | | | : : | : | | : | : | : | : | : | : | :
Db     138 HVVFALRARTVTFGIISSIITWVLAALVSIPCLYVFKSQMEFTYHTCRAILPRKSLIRFL 197

Qy     200 NFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVYFLFWTPY 259
      | : | | | | : | | | | : | | | : | | | | : | : | : | : | : |
Db     198 RFQALTMNIGLILP LLAMIICYTRIINVLRH-RPNKKKAKVMRLIFVITLLFFLLLPY 256

Qy     260 NIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVF 319
      : : : | : : : | : | : : | | | | | | : | | | : | : | : |
Db     257 YLAAFVSAFEDVLFTPSCLRSQQVDLSLMITEALAYTHCCVNPVIYVFVGKRFRKYLWQL 316

Qy     320 FRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      | | : | : | | | | | | | | | | | | |
Db     317 FRRHTAITLPQWLP-FLSEDRAQRASARLPSTVEIETSADL 356
```

# RESULT 12

JC5067

G protein-coupled receptor CKR-L1 - human

N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jul-2000

C;Accession: JC5067; G02776; G02387

R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

A;Reference number: JC5067; MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA

A;Residues: 1-355 <ZAB>

A;Cross-references: EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736

R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.

submitted to the EMBL Data Library, June 1996

A;Reference number: H01714

A;Accession: G02776

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <NAP>

A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979  
 R;Bonner, T.I.  
 submitted to the EMBL Data Library, January 1996  
 A;Reference number: H01154  
 A;Accession: G02387  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-355 <BON>  
 A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057  
 C;Comment: This protein belongs to the family of beta chemokine receptors.  
 C;Genetics:  
 A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1  
 A;Cross-references: GDB:6053733; OMIM:601834  
 A;Map position: 3p21-3p21  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; transmembrane protein  
 F;36-63/Domain: transmembrane #status predicted <TM1>  
 F;73-94/Domain: transmembrane #status predicted <TM2>  
 F;108-129/Domain: transmembrane #status predicted <TM3>  
 F;147-171/Domain: transmembrane #status predicted <TM4>  
 F;200-222/Domain: transmembrane #status predicted <TM5>  
 F;239-260/Domain: transmembrane #status predicted <TM6>  
 F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 39.5%; Score 751; DB 2; Length 355;  
 Best Local Similarity 41.2%; Pred. No. 2.1e-56;  
 Matches 143; Conservative 69; Mismatches 121; Indels 14; Gaps 5;

```

Qy      20 VTTFFDYDY----GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
      ||| || | :|| :: | || | ||:| | :|| ||:|:|: ||||:
Db      9 VTTVTDYYPDIFSSPCDAELIQTNGLKLLAVFYCLLFVFSLLGNLSLVILVVLVCKKLRS 68

Qy      76 LTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT 135
      :||:|||||:||||: : | : :||| |||: :| |:|:|: ||| |:|
Db      69 ITDVYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSFGFYIYGFYSSMFFITLMS 128

Qy     136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
      :|||||:||||:||| ||: | : || |: |:| :| : || | | :|
Db     129 VDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGLVLCYSFYN 188

Qy     196 R---GWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVY 252
      : | | ||||:| | : || || | ||:| | :|:|:| :|
Db     189 QQTLKWKIFTNFKMNI LGLLPFTIFMFCYIKILHQLKRCQNHNKT-KAIRLVLI VVIAS 247

Qy     253 FLFWTPYNI VILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF 312
      ||| |:|:|: | : | | : || || ||| : ||||:|:|:|||||
Db     248 LLFWVPFN VVLF LTLSHSMHILDGCSI SQQLT YATHVTEIISFTHCCVNPVIYAFVGEKF 307

Qy     313 RRYLSVFFRKHITKRF---CKQCPVFYRETVDGVTSTNTPSTGEQEV 356
      ::|| |:| :| :| | ||| :| :| :| :| :|
Db     308 KHLSEIFQKSCSQIFNYLGRQMP---RESCEKSSSCQQHSSRSSSV 351

```

RESULT 13  
 I58186  
 probable G protein-coupled receptor - rat  
 C;Species: Rattus norvegicus (Norway rat)



C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
 C;Accession: I58186  
 R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.  
 Neurosci. Lett. 169, 85-89, 1994  
 A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal  
 cord and brain related to chemokine receptors.  
 A;Reference number: I58186; MUID:94323113; PMID:8047298  
 A;Accession: I58186  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-354 <RES>  
 A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor

Query Match 38.0%; Score 722.5; DB 2; Length 354;  
 Best Local Similarity 46.2%; Pred. No. 5.5e-54;  
 Matches 160; Conservative 46; Mismatches 121; Indels 19; Gaps 8;

```

Qy      24 FDYDYG-A-PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLL 82
      |:|| | |: | | |||| | |||:|||| | |:| :|||||
Db      13 FEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVLALTNSRKSITSITDIYLL 72

Qy      83 NLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAI 142
      |||:|||||: ||| | | : ||||| | : ||:||||||| ::|||
Db      73 NLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTATFFFIGFFGGIFFITVISIDRYLAI 132

Qy     143 VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRGWNNFH 202
      | | :: ||| || |: | |: | :||| ::: | :|
Db     133 VLAANSMNRTVQHGVTSISLGVWAAAILVASPQFMFTK-RKDNE---CLGDYPEVLQEIW 188

Qy     203 TIMR---NILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLFWTP 258
      ::| ||| ||||| || |::|| |:| || ||:|:| ::|:|||||
Db     189 PVLNRNSEVNILGFVLPLLIMSFCYFRIVRTLFSCKNRKKA-RAIRLILLVVVVFFLEFWTP 247

Qy     259 YNIVILLNTFQEFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSV 318
      ||||| | | : : :| | | ||||: :|||:| ||| |||||
Db     248 YNIVIFLETLKFYNFFPSCGMKRDRLWALSVTETVAFSHCCLNPFIIYAFAGEKFRRYLRH 307

Qy     319 FFRKHITKRFCQKQCPVF-----YRETVDGVTSTNTPSTGEQEV 357
      : | : | : || | | : | : | | | |
Db     308 LYNKCLAV-LCGR-PVHAGFSTESQRSRQDSILSSLTHYTSEGE 351
  
```

#### RESULT 14

JC4304  
 orphan G protein-coupled receptor - human  
 N;Alternate names: V28 protein  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 19-May-2000  
 C;Accession: JC4304  
 R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.  
 Gene 163, 295-299, 1995  
 A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely  
 related to genes for chemokine receptors and is expressed in lymphoid and  
 neural tissues.  
 A;Reference number: JC4304; MUID:96011651; PMID:7590284

A;Accession: JC4304  
 A;Molecule type: mRNA  
 A;Residues: 1-355 <RAP>  
 A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581  
 A;Experimental source: peripheral blood mononuclear cell  
 C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.  
 C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.  
 C;Genetics:  
 A;Gene: v28  
 A;Map position: 3pter-p21  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein  
 F;35-57/Domain: transmembrane #status predicted <TM1>  
 F;66-88/Domain: transmembrane #status predicted <TM2>  
 F;104-125/Domain: transmembrane #status predicted <TM3>  
 F;146-165/Domain: transmembrane #status predicted <TM4>  
 F;197-217/Domain: transmembrane #status predicted <TM5>  
 F;230-254/Domain: transmembrane #status predicted <TM6>  
 F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 37.3%; Score 708; DB 2; Length 355;  
 Best Local Similarity 46.8%; Pred. No. 9.5e-53;  
 Matches 145; Conservative 47; Mismatches 108; Indels 10; Gaps 5;

Qy	18	EEVTTFFDY-DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCL	76
		:       :             :           :	
Db	6	ESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSV	65
Qy	77	TDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTI	136
		:                               :	
Db	66	TDIYLLNLALSDLLFVATLPPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFFITVISI	125
Qy	137	DRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR	196
		:                 :     :           :     :	
Db	126	DRYLAI VLAANSNMNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE	181
Qy	197	GWNNFHTIMRNI----LGLVLP LLIMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVY	252
		:     :                     :         :     :     :     :     :	
Db	182	VLQEIWPVLRNVETNFLGFLPLLLIMSYCYFRIIQTLFSCKNHKKK-KAIKLILLVVIVF	240
Qy	253	FLFWTPYNI VILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF	312
		:       : : :           : :     :     :	
Db	241	FLFWTPYNMIFLETCLKLYDFFPSCDMRDKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF	300
Qy	313	RRYLSVFFRK	322
		:	
Db	301	RRLYHLYGK	310

RESULT 15

JC5942

chemokine receptor - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000

C;Accession: JC5942  
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.  
Biochem. Biophys. Res. Commun. 243, 264-268, 1998  
A;Title: Cloning and characterization of a novel human chemokine receptor.  
A;Reference number: JC5942; MUID:98139902; PMID:9473515  
A;Accession: JC5942  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-344 <FAN>  
A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071  
C;Superfamily: vertebrate rhodopsin

Query Match 34.2%; Score 649.5; DB 2; Length 344;  
Best Local Similarity 43.0%; Pred. No. 8.7e-48;  
Matches 128; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

Qy	27	DYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGNMLVVLILINCKKLKCLTDIYLLNLAI	86
Db	23	DEAEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAV	82
Qy	87	SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLAIVH-A	145
Db	83	SNLCFLLTLPLFWAHAG-----GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKG	136
Qy	146	VFALKARTVTFGVVTSVITWLVAVFASVPGI IFTKCQKEDSVYVCG----PYFPRG---W	198
Db	137	NFFSARRRVPCGIITSVLAWVTAILATLPEYVVYKPKMEDQKYKCAFSRTPFLPADETFW	196
Qy	199	NNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWTP	258
Db	197	KHFLTLKMNISVLVLP LFI FTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLLMWAP	253
Qy	259	YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYL	316
Db	254	YNIAFFLSTFKEHFSLS DCKSSYNLDKSVHITKLIATTHCCINPLLYAFLDGTF SKYL	311

Search completed: November 25, 2003, 23:21:06  
Job time : 21 secs

OM protein - protein search, using sw model

Run on: November 25, 2003, 23:04:24 ; Search time 18 Seconds  
 (without alignments)  
 940.534 Million cell updates/sec

Title: US-09-625-573-4  
 Perfect score: 1900  
 Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNPSTGEQEVSA GL 360

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1845	97.1	360	1	CKR2_MACMU	018793 macaca mula
2	1651.5	86.9	374	1	CKR2_HUMAN	P41597 homo sapien
3	1542	81.2	373	1	CKR2_RAT	055193 rattus norv
4	1535	80.8	373	1	CKR2_MOUSE	P51683 mus musculu
5	1396	73.5	354	1	CKR5_MOUSE	P51682 mus musculu
6	1386	72.9	354	1	CKR5_RAT	008556 rattus norv
7	1376	72.4	352	1	CKR5_CERTO	062743 cercocobus
8	1371	72.2	352	1	CKR5_HYLLE	097883 hylobates 1
9	1370	72.1	352	1	CKR5_MACMU	P79436 macaca mula
10	1370	72.1	352	1	CKR5_PANTR	P56440 pan troglod
11	1370	72.1	352	1	CKR5_PONPY	097881 pongo pygma
12	1368	72.0	352	1	CKR5_GORGO	P56439 gorilla gor
13	1368	72.0	352	1	CKR5_PAPHA	P56441 papio hamad
14	1364	71.8	352	1	CKR5_HUMAN	P51681 homo sapien
15	1363	71.7	352	1	CKR5_TRAPH	097879 trachypithe
16	1361	71.6	352	1	CKR5_PYGBI	097880 pygathrix b
17	1360	71.6	352	1	CKR5_TRAFR	097878 trachypithe

18	1359	71.5	352	1	CKR5_PYGNE	097882	pygathrix n
19	1344	70.7	352	1	CKR5_CERAE	P56493	cercopithec
20	1036	54.5	355	1	CKR1_HUMAN	P32246	homo sapien
21	1018.5	53.6	359	1	CKR3_MOUSE	P51678	mus musculu
22	1003.5	52.8	359	1	CKR3_RAT	O54814	rattus norv
23	995	52.4	358	1	CKR3_CAVPO	Q9z2i3	cavia porce
24	981	51.6	355	1	CKR1_MACMU	P56482	macaca mula
25	960.5	50.6	355	1	CKR1_MOUSE	P51675	mus musculu
26	947	49.8	355	1	CKR3_HUMAN	P51677	homo sapien
27	940.5	49.5	355	1	CKR3_MACMU	P56483	macaca mula
28	924.5	48.7	355	1	CKR3_CERAE	P56492	cercopithec
29	871	45.8	360	1	CKR4_MOUSE	P51680	mus musculu
30	862.5	45.4	360	1	CKR4_HUMAN	P51679	homo sapien
31	778.5	41.0	356	1	CKRV_MOUSE	P51676	mus musculu
32	751	39.5	355	1	CKR8_HUMAN	P51685	homo sapien
33	743.5	39.1	356	1	CKR8_MACMU	O97665	macaca mula
34	731.5	38.5	353	1	CKR8_MOUSE	P56484	mus musculu
35	722.5	38.0	354	1	C3X1_RAT	P35411	rattus norv
36	715.5	37.7	354	1	C3X1_MOUSE	Q9z0d9	mus musculu
37	708	37.3	355	1	C3X1_HUMAN	P49238	homo sapien
38	599	31.5	384	1	CKD6_HUMAN	O00590	homo sapien
39	595	31.3	378	1	CKD6_MOUSE	O08707	mus musculu
40	591	31.1	382	1	CKD6_RAT	O09027	rattus norv
41	581.5	30.6	378	1	CKR7_HUMAN	P32248	homo sapien
42	575	30.3	357	1	CKR9_HUMAN	P51686	homo sapien
43	571.5	30.1	367	1	CKR6_MOUSE	O54689	mus musculu
44	569	29.9	369	1	CKR9_MOUSE	Q9wut7	mus musculu
45	569	29.9	378	1	CKR7_MOUSE	P47774	mus musculu

# ALIGNMENTS

## RESULT 1

### CKR2\_MACMU

ID CKR2\_MACMU STANDARD; PRT; 360 AA.  
AC O18793;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)  
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
GN CCR2 OR CMKBR2.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21354176; PubMed=11461684;  
RA Margulies B.J., Hauer D.A., Clements J.E.;  
RT "Identification and comparison of eleven rhesus macaque chemokine  
RT receptors.";  
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
CC -!- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.  
CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS

```

CC      LEVEL.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC          Name=B;
CC          IsoId=O18793-1; Sequence=Displayed;
CC          Name=A;
CC          IsoId=O18793-2; Sequence=Not described;
CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF013958; AAD11572.1; -.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW      Alternative splicing.
FT      DOMAIN      1      42      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM     43      70      1 (POTENTIAL).
FT      DOMAIN      71      80      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM     81     100      2 (POTENTIAL).
FT      DOMAIN     101     114      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM     115     136      3 (POTENTIAL).
FT      DOMAIN     137     153      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM     154     178      4 (POTENTIAL).
FT      DOMAIN     179     206      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM     207     226      5 (POTENTIAL).
FT      DOMAIN     227     243      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM     244     268      6 (POTENTIAL).
FT      DOMAIN     269     285      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM     286     309      7 (POTENTIAL).
FT      DOMAIN     310     360      CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD      14      14      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      MOD_RES       26      26      SULFATION (BY SIMILARITY).
FT      DISULFID     113     190      BY SIMILARITY.
SQ      SEQUENCE    360 AA;  41139 MW;  4B2552BCE913FE9F CRC64;

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Query Match          97.1%;  Score 1845;  DB 1;  Length 360;
Best Local Similarity 96.9%;  Pred. No. 9e-105;
Matches 349;  Conservative 5;  Mismatches 6;  Indels 0;  Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

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Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR	240
		:     :	
Db	181	CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTSQ LDQATQVTETLGMTHCCI	300
		:	
Db	241	AVRLIFTIMIVYFLFWTPYNI VILLNTFQEFFGLSNCESTRQ LDQATQVTETLGMTHCCI	300
Qy	301	NP I IYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360
		:	
Db	301	NP I IYAFVGEKFRRYLSMFFRKYITKR FCKQCPVFYRETVDGVTSTNTPSTAEQEV SVGL	360

## RESULT 2

### CKR2\_HUMAN

ID CKR2\_HUMAN STANDARD; PRT; 374 AA.

AC P41597;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)

DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).

GN CCR2 OR CMKBR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94195821; PubMed=8146186;

RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,

RA Coughlin S.R.;

RT "Molecular cloning and functional expression of two monocyte

RT chemoattractant protein 1 receptors reveals alternative splicing of

RT the carboxyl-terminal tails.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=94324942; PubMed=8048929;

RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;

RT "cDNA cloning and functional expression of a human monocyte

RT chemoattractant protein 1 receptor.";

RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97150864; PubMed=8995400;

RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;

RT "Organization and differential expression of the human monocyte

RT chemoattractant protein 1 receptor gene. Evidence for the role of the

RT carboxyl-terminal tail in receptor trafficking.";

RL J. Biol. Chem. 272:1038-1045(1997).

RN [4]

RP SEQUENCE FROM N.A.  
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,  
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,  
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,  
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.  
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,  
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.  
 RX MEDLINE=20501139; PubMed=11046064;  
 RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
 RA Chakravarty L., Kolattukudy P.E.;  
 RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
 RT has tyrosine sulfation in a conserved extracellular N-terminal  
 RT region.";  
 RL J. Immunol. 165:5295-5303(2000).  
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=A;  
 CC IsoId=P41597-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=P41597-2; Sequence=VSP\_001893;  
 CC -!- PTM: N-GLYCOSYLATED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; U03882; AAA19119.1; -.  
 DR EMBL; U03905; AAA19120.1; -.  
 DR EMBL; D29984; BAA06253.1; -.  
 DR EMBL; U80924; AAC51637.1; -.  
 DR EMBL; U80924; AAC51636.1; -.  
 DR EMBL; U95626; AAB57791.1; -.  
 DR EMBL; U95626; AAB57792.1; -.  
 DR EMBL; AF545480; AAN16400.1; -.  
 DR PIR; I38450; I38450.  
 DR PIR; JC2443; JC2443.  
 DR PDB; 1KAD; 14-AUG-02.  
 DR PDB; 1KP1; 23-JAN-02.  
 DR Genew; HGNC:1603; CCR2.



DR MIM; 601267; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005625; C:soluble fraction; TAS.

DR GO; GO:0004950; F:chemokine receptor activity; TAS.

DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.

DR GO; GO:0006968; P:cellular defense response; TAS.

DR GO; GO:0006935; P:chemotaxis; TAS.

DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR GO; GO:0007125; P:invasive growth; TAS.

DR GO; GO:0007259; P:JAK-STAT cascade; TAS.

DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;

KW Polymorphism; Alternative splicing; 3D-structure.

FT	DOMAIN	1	42	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	43	70	1 (POTENTIAL).
FT	DOMAIN	71	80	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	81	100	2 (POTENTIAL).
FT	DOMAIN	101	114	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	115	136	3 (POTENTIAL).
FT	DOMAIN	137	153	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	154	178	4 (POTENTIAL).
FT	DOMAIN	179	206	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	207	226	5 (POTENTIAL).
FT	DOMAIN	227	243	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	244	268	6 (POTENTIAL).
FT	DOMAIN	269	285	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	286	309	7 (POTENTIAL).
FT	DOMAIN	310	374	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	26	26	SULFATION.
FT	DISULFID	113	190	BY SIMILARITY.
FT	VARSPPLIC	314	374	SLFHIALGCRIAPLQKPVCGPGVRPGKNVKVTTQGLLDGR
FT				GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
FT				QCPVFYRETVDGVTSTNTPSTGEQEVSAAGL (in
FT				isoform B).
FT				/FTId=VSP_001893.
FT	VARIANT	64	64	V -> I (IN dbSNP:1799864).
FT				/FTId=VAR_014339.
FT	VARIANT	355	355	G -> E.
FT				/FTId=VAR_014340.
SQ	SEQUENCE	374 AA;	41914 MW;	F865E0D39E74CF0F CRC64;

Query Match 86.9%; Score 1651.5; DB 1; Length 374;

Best Local Similarity 95.5%; Pred. No. 4.2e-93;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY	120



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DR      EMBL; U77349; AAC03242.1; -.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane.
FT      DOMAIN          1          60          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        61          81          POTENTIAL.
FT      DOMAIN          82          91          CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        92         112          POTENTIAL.
FT      DOMAIN         113         128          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM       129         149          POTENTIAL.
FT      DOMAIN         150         170          CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM       171         191          POTENTIAL.
FT      DOMAIN         192         220          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM       221         241          POTENTIAL.
FT      DOMAIN         242         256          CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM       257         277          POTENTIAL.
FT      DOMAIN         278         301          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM       302         322          POTENTIAL.
FT      DOMAIN         323         373          CYTOPLASMIC (POTENTIAL).
FT      DISULFID        126         203          BY SIMILARITY.
SQ      SEQUENCE        373 AA;  42763 MW;  2E7BB012F5D6FD09 CRC64;

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Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
		:          :       :                :	
Db	14	ILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN	73
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY	120
		::   :      :                 :	
Db	74	MLVIIILISCKKLKSMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGLY	133
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTK	180
		:   :   :     :	
Db	134	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTTFGVITSVVTWVAVFASLPGIIFTK	193
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRCRNEKKRHR	240
		:    :                 :   :	
Db	194	SEQEDDQHTCGPYFPPTIWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRRCRNEKKRHR	253
Qy	241	AVRVIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
		:               :         :                     :	
Db	254	AVRLIFAIMIVYFLFWTPYINIVLFLTTFQEFGLGMSNCVDMHLDQAMQVTETLGMTHCCV	313
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
		:                        :	
Db	314	NPIIYAFVGEKFRRYLSIFFRKHIANKLCKQCPVFYRETADRVSSSTFTSTGEQEVSVGL	373

# RESULT 4

## CKR2\_MOUSE

ID CKR2\_MOUSE STANDARD; PRT; 373 AA.

AC P51683; Q61172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)

DE (JE/FIC receptor) (MCP-1 receptor).

GN CCR2 OR CMKBR2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96205938; PubMed=8631787;

RA Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,

RA Charo I.F.;

RT "Molecular cloning and functional expression of murine JE (monocyte

RT chemoattractant protein 1) and murine macrophage inflammatory protein

RT 1alpha receptors: evidence for two closely linked C-C chemokine

RT receptors on chromosome 9.";

RL J. Biol. Chem. 271:7551-7558(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=96216064; PubMed=8662823;

RA Kurihara T., Bravo R.;

RT "Cloning and functional expression of mCCR2, a murine receptor for

RT the C-C chemokines JE and FIC.";

RL J. Biol. Chem. 271:11603-11606(1996).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97026720; PubMed=8872898;

RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,

RA Post T.W., Gerard C., Dorf M.E.;

RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse

RT transcriptase-polymerase chain reaction does not detect mRNA for the

RT KC or new MCP-1 receptor.";

RL J. Neurosci. Res. 45:382-391(1996).

CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5

CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR

CC CALCIUM IONS LEVEL.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,

CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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```

Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||:|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      254 AVRLLFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDDQAMQVTETLGMTHCCI 313

Qy      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
      ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      314 NPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPVFYRETADRVSSSTFTPSTGEQEVSVGL 373

```

# RESULT 5

## CKR5\_MOUSE

```

ID      CKR5_MOUSE      STANDARD;      PRT;      354 AA.
AC      P51682; O35313; O35891; P97308; P97405; Q61867;
DT      01-OCT-1996 (Rel. 34, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE      alpha receptor).
GN      CCR5 OR CMKBR5.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvJ; TISSUE=Spleen;
RX      MEDLINE=96205938; PubMed=8631787;
RA      Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA      Charo I.F.;
RT      "Molecular cloning and functional expression of murine JE (monocyte
RT      chemoattractant protein 1) and murine macrophage inflammatory protein
RT      1alpha receptors: evidence for two closely linked C-C chemokine
RT      receptors on chromosome 9.";
RL      J. Biol. Chem. 271:7551-7558(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX      MEDLINE=96278910; PubMed=8662890;
RA      Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT      "Cloning and characterization of a novel murine macrophage
RT      inflammatory protein-1 alpha receptor.";
RL      J. Biol. Chem. 271:14445-14451(1996).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/Ola;
RA      Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL      Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX      MEDLINE=98001387; PubMed=9343222;
RA      Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT      "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT      implicate specific amino acids in infections by simian and human
RT      immunodeficiency viruses.";
RL      J. Virol. 71:8642-8656(1997).

```

RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=97404635; PubMed=9261347;  
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,  
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;  
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human  
 RT immunodeficiency virus type 1.";  
 RL J. Virol. 71:6305-6314(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Guo B., Kuno K., Harada A., Matsushima K.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,  
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U47036; AAC52454.1; -.  
 DR EMBL; X94151; CAA63867.1; -.  
 DR EMBL; U68565; AAB37273.1; -.  
 DR EMBL; U83327; AAC53386.1; -.  
 DR EMBL; AF022990; AAC53389.1; -.  
 DR EMBL; AF019772; AAB71183.1; -.  
 DR EMBL; D83648; BAA12024.1; -.  
 DR MGD; MGI:107182; Ccr5.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.  
 DR GO; GO:0006952; P:defense response; IMP.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 33 60 1 (POTENTIAL).  
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 71 91 2 (POTENTIAL).  
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 105 126 3 (POTENTIAL).  
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 144 168 4 (POTENTIAL).  
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 201 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 262 6 (POTENTIAL).

FT	DOMAIN	263	279	EXTRACELLULAR (POTENTIAL) .
FT	TRANSMEM	280	303	7 (POTENTIAL) .
FT	DOMAIN	304	354	CYTOPLASMIC (POTENTIAL) .
FT	DISULFID	103	180	BY SIMILARITY .
FT	CARBOHYD	270	270	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	VARIANT	11	11	I -> S .
FT	VARIANT	62	62	K -> R .
FT	VARIANT	66	66	V -> M .
FT	VARIANT	97	97	I -> V .
FT	VARIANT	109	109	V -> L .
FT	VARIANT	156	156	V -> A .
FT	VARIANT	160	160	F -> S .
FT	VARIANT	185	185	P -> L .
FT	VARIANT	213	213	I -> V .
FT	VARIANT	318	318	I -> M .
FT	VARIANT	337	337	V -> A .
FT	CONFLICT	3	3	F -> L (IN REF. 2) .
FT	CONFLICT	80	80	L -> F (IN REF. 2) .
FT	CONFLICT	145	145	N -> Y (IN REF. 5) .
FT	CONFLICT	190	190	H -> I (IN REF. 3) .
FT	CONFLICT	208	208	P -> S (IN REF. 1) .
SQ	SEQUENCE	354 AA;	40863 MW;	B4A6B942E88F9CF0 CRC64;

Query Match 73.5%; Score 1396; DB 1; Length 354;  
Best Local Similarity 74.6%; Pred. No. 9.7e-78;  
Matches 261; Conservative 33; Mismatches 50; Indels 6; Gaps 2;

Qy	17	GEEVTTFFDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMMLVVLILINCKKLK	74
		:           :                             :         :	
Db	5	GSVPTYIYDIDYGMSAPCQKINVKQIAAQLLPPLYSLVFIFGFVGNMMLVVLILISCKKLK	64
Qy	75	CLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL	134
		:                         :             :         :     :	
Db	65	SVTDIYLLNLAI SDLLFLLTLPLFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFFIILL	124
Qy	135	TIDRYLAI VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTCKQKEDSVYVCGPYF	194
		:     :     :         :         :         :	
Db	125	TIDRYLAI VHAVFALKVRTVNFVITSVVTVWVAVFASLPEIIFTRSQKEGFHYTCSPHF	184
Qy	195	PRG---WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMI	250
		:   :     :       :   :                         :	
Db	185	PHTQYHFWKSFQTLKMVILSLILPLLVMII CYSGILHTLFCRNEKKRHRRAVRILFAIMI	244
Qy	251	VYFLFWTPYNI VILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE	310
		:                 :     :                 :	
Db	245	VYFLFWTPYNI VLLLTTFQEFFGLNNCSSNRLDQAMQATETLGMTHCCINPVIYAFVGE	304
Qy	311	KFRRLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
		:   :   :     :	
Db	305	KFRSYLSVFFRKHIVKRFCRCSIFOODNPDRVSSVYTRSTGEHEVSTGL	354

```

RESULT 6
CKR5_RAT
ID      CKR5_RAT      STANDARD;      PRT;      354 AA.
AC      008556;
DT      01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1  
 DE alpha receptor).  
 GN CCR5 OR CMKBR5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Brain;  
 RX MEDLINE=98334064; PubMed=9670989;  
 RA Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,  
 RA Berger M., Gebicke-Haerter P.J.;  
 RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and  
 RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";  
 RL J. Neurosci. Res. 53:16-28(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis.";  
 RL J. Neuroimmunol. 86:1-12(1998).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; Y12009; CAA72737.1; -.  
 DR EMBL; U77350; AAC03243.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 33 60 1 (POTENTIAL).  
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 71 91 2 (POTENTIAL).  
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 105 126 3 (POTENTIAL).  
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 144 168 4 (POTENTIAL).

FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 201 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 262 6 (POTENTIAL).  
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 280 303 7 (POTENTIAL).  
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 103 180 BY SIMILARITY.  
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 72.9%; Score 1386; DB 1; Length 354;  
 Best Local Similarity 74.9%; Pred. No. 3.9e-77;  
 Matches 262; Conservative 30; Mismatches 52; Indels 6; Gaps 2;

Qy 17 GEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK 74  
 | | : | | | | | : | | | | | | | | | | | | | | | | : | | | | : | | | |  
 Db 5 GSIPTYIYDIDYSMSAPCQKVNKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISCKKLK 64  
  
 Qy 75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL 134  
 : | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 65 SMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGIYHIGYFGGIFFIILL 124  
  
 Qy 135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF 194  
 | | | | | | | | | | : | | | | | | : | | : | | : | | | | : | | | | : | | | |  
 Db 125 TIDRYLAIVHAVFAIKARTVNFGVITSVVTVWVAVFVSLPEIIFMRSQKEGSHYTCSPHF 184  
  
 Qy 195 ----PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMI 250  
 | | : | | : | | : | | : | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 185 LHIQYRFWKHFQTLKMVILSLILPLVMVICYSGILNTLFRCRNEKKRHRAVRLIFAIMI 244  
  
 Qy 251 VYFLFWTPYNIVILLNTFQEYFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE 310  
 | | | | | | | | | | : | | | | | | : | | : | | : | | | | | | | | | | | | | | | |  
 Db 245 VYFLFWTPYNIVLLLTTFQEYFGLNNCSSSNRLDQAMQVTETLGMTHCCLNPVIYAFVGE 304  
  
 Qy 311 KFRRYLSVFFRKHITKRFCQKCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360  
 | | | | | | | | | | | | | | : | : | : | | | | | | | | | | | | | | | | | | |  
 Db 305 KFRNYLSVFFRKHIVKRFCCKHCSIFQQVNPDRVSSVYTRSTGEQEVSTGL 354

# RESULT 7

## CKR5\_CERTO

ID CKR5\_CERTO STANDARD; PRT; 352 AA.  
 AC O62743; O62744; O62745; O62746;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate 079, 085, 087, and 089;

```

RX  MEDLINE=98321155; PubMed=9656999;
RA  Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT  "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT  naturally infected in west Africa: a comparison of coreceptor usage
RT  of primary SIVsm, HIV-2, and SIVmac.";
RL  Virology 246:113-124(1998).
CC  -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC      MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC      INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC      IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC      DIFFERENTIATION.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC  -----
DR  EMBL; AF051902; AAC39830.1; -.
DR  EMBL; AF051903; AAC39831.1; -.
DR  EMBL; AF051904; AAC39832.1; -.
DR  EMBL; AF051905; AAC39833.1; -.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRRHODOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT  DOMAIN          1      30      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM        31      58      1 (POTENTIAL).
FT  DOMAIN          59      68      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM        69      89      2 (POTENTIAL).
FT  DOMAIN          90     102      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM       103     124      3 (POTENTIAL).
FT  DOMAIN         125     141      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM       142     166      4 (POTENTIAL).
FT  DOMAIN         167     198      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM       199     218      5 (POTENTIAL).
FT  DOMAIN         219     235      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM       236     260      6 (POTENTIAL).
FT  DOMAIN         261     277      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM       278     301      7 (POTENTIAL).
FT  DOMAIN         302     352      CYTOPLASMIC (POTENTIAL).
FT  DISULFID        101     178      BY SIMILARITY.
FT  MOD_RES          3       3      SULFATION (BY SIMILARITY).
FT  MOD_RES         10      10      SULFATION (BY SIMILARITY).
FT  MOD_RES         14      14      SULFATION (BY SIMILARITY).
FT  MOD_RES         15      15      SULFATION (BY SIMILARITY).
FT  VARIANT          2       2      D -> E (IN ISOLATE 087).
FT  VARIANT          3       3      Y -> D (IN ISOLATE 079).
FT  VARIANT         25      25      V -> G (IN ISOLATE 087).
FT  VARIANT        100     100      M -> K (IN ISOLATE 079).
FT  VARIANT        107     107      L -> V (IN ISOLATE 089).

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FT VARIANT 134 134 V -> G (IN ISOLATE 079).  
 FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).  
 FT VARIANT 340 340 T -> I (IN ISOLATE 079).  
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 72.4%; Score 1376; DB 1; Length 352;  
 Best Local Similarity 76.4%; Pred. No. 1.5e-76;  
 Matches 262; Conservative 31; Mismatches 44; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
 :| || || | :||| |:|||||||||||||||:|||||||||:| :|||  
 Db 10 YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69  
 Qy 82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
 |||||:|:| || | :| || | |:| ||| |:| ||||| |||||  
 Db 70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129  
 Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197  
 |||||:|||||:|||||:|:| | | |:| :  
 Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSPHPYSQYQF 189  
 Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRVRIFTIMIVYFLFWT 257  
 | || |: |||||:|||||:|||||:|||||:|||||  
 Db 190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLRLCRNEKKRHRVRLIFTIMIVYFLFWA 249  
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
 ||||:|||||:| |::||| |||||:|||||:| |  
 Db 250 PYNIVLLLNTFQEFFGLNCCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309  
 Qy 318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360  
 ||:| || ||| | :| :| :| | |||||:| ||  
 Db 310 VFFQKHIKRFCCKCSIFQQEASERASSVYTRSTGEQEISVGL 352

# RESULT 8

CKR5\_HYLLE

ID CKR5\_HYLLE STANDARD; PRT; 352 AA.

AC O97883;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).

GN CCR5 OR CMKBR5.

OS Hylobates leucogenys (White-cheeked gibbon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI\_TaxID=61853;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99416438; PubMed=10486970;

RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";

RL Mol. Biol. Evol. 16:1145-1154(1999).

CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR

CC DIFFERENTIATION.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL; AF075451; AAD19863.1; -.

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218 5 (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).

FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).

SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 72.2%; Score 1371; DB 1; Length 352;

Best Local Similarity 76.2%; Pred. No. 3.1e-76;

Matches 259; Conservative 30; Mismatches 47; Indels 4; Gaps 1;

Qy 25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84

Db 13 DYDTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILVLINCKRLKSMTDIYLLNL 72

Qy 85 AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH 144

Db 73 AISDLFFLLTVPFWAHYAAQWDFGNTMCQLLTGLYFIGFFSFIGFFIILLTIDRYLAIVH 132

Qy 145 AVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RGWNN 200

Db 133 AVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHFPPYSQYQFWKN 192

Qy 201 FHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLFWTPYN 260

```

      | | : | | | | | | | | : | | | | | | | | | | | | | | | | | : | | | | | | | | | | | |
Db      193 FQTLKIVILGLVLP LLVMVICYSGILKTL LRCRNEKKRHRAVRLIFTIMIVYFLFWAPYN 252

QY      261 IVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFF 320
      | | : | | | | | | | | | | | | : | | : | | | | | | | | | | | | | | | | | | | | |
Db      253 IVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312

QY      321 RKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      : | | | | | | | | : | : | : | : | | | | | | : | |
Db      313 QKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352

```

# RESULT 9

## CKR5\_MACMU

```

ID      CKR5_MACMU      STANDARD;      PRT;      352 AA.
AC      P79436; O02746;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN      CCR5 OR CMKBR5.
OS      Macaca mulatta (Rhesus macaque),
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS      Macaca nemestrina (Pig-tailed macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544, 9541, 9545;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SPECIES=M.mulatta;
RX      MEDLINE=97184592; PubMed=9032394;
RA      Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA      Newman W., Gerard N., Gerard C., Sodroski J.;
RT      "Utilization of C-C chemokine receptor 5 by the envelope
RT      glycoproteins of a pathogenic simian immunodeficiency virus,
RT      SIVmac239.";
RL      J. Virol. 71:2522-2527(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES=M.mulatta; STRAIN=Indian macaque;
RX      MEDLINE=97213934; PubMed=9060623;
RA      Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT      "Genetically divergent strains of simian immunodeficiency virus use
RT      CCR5 as a coreceptor for entry.";
RL      J. Virol. 71:2705-2714(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      SPECIES=M.mulatta;
RX      MEDLINE=21354176; PubMed=11461684;
RA      Margulies B.J., Hauer D.A., Clements J.E.;
RT      "Identification and comparison of eleven rhesus macaque chemokine
RT      receptors.";
RL      AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;

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RX  MEDLINE=97268687; PubMed=9108095;
RA  Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA  Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA  Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT  "Differential utilization of CCR5 by macrophage and T cell tropic
RT  simian immunodeficiency virus strains.";
RL  Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC  -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC      MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC      INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC      IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC      DIFFERENTIATION.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U77672; AAC51109.1; -.
DR  EMBL; U73739; AAC51158.1; -.
DR  EMBL; U96762; AAC34132.1; -.
DR  EMBL; AF005660; AAB62554.1; -.
DR  EMBL; AF005661; AAB62555.1; -.
DR  EMBL; AF005662; AAB62556.1; -.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRRHODOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT  DOMAIN      1      30      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM     31     58      1 (POTENTIAL).
FT  DOMAIN      59     68      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM     69     89      2 (POTENTIAL).
FT  DOMAIN      90    102      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM    103    124      3 (POTENTIAL).
FT  DOMAIN     125    141      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM    142    166      4 (POTENTIAL).
FT  DOMAIN     167    198      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM    199    218      5 (POTENTIAL).
FT  DOMAIN     219    235      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM    236    260      6 (POTENTIAL).
FT  DOMAIN     261    277      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM    278    301      7 (POTENTIAL).
FT  DOMAIN     302    352      CYTOPLASMIC (POTENTIAL).
FT  DISULFID    101    178      BY SIMILARITY.
FT  MOD_RES       3       3      SULFATION (BY SIMILARITY).
FT  MOD_RES      10      10      SULFATION (BY SIMILARITY).
FT  MOD_RES      14      14      SULFATION (BY SIMILARITY).
FT  MOD_RES      15      15      SULFATION (BY SIMILARITY).
FT  CARBOHYD    268    268      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CONFLICT    241    241      M -> I (IN REF. 3).

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FT CONFLICT 292 292 I -> M (IN REF. 3).  
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 72.1%; Score 1370; DB 1; Length 352;  
Best Local Similarity 76.1%; Pred. No. 3.5e-76;  
Matches 261; Conservative 31; Mismatches 45; Indels 6; Gaps 2;

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Qy      24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| ||      || | :||| |:|||||:|||||:|||||:|||||:|||||
Db      10 YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69

Qy      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      |||||:|||:||| || | :| || | ||| ||| ||| ||| ||| ||| |||
Db      70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy     142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHFPYSQYQF 189

Qy     198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
      || | |: |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     190 WKNFQTLKMOVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWA 249

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      |||||:|||||:|||||:||| :::||| |||||:|||||:|||||:|||||
Db     250 PYNIVLLNTFQEFFGLNNCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy     318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      |||:||| |||| | :| : | : | |||||:|| ||
Db     310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 10

CKR5\_PANTR

ID CKR5\_PANTR STANDARD; PRT; 352 AA.  
AC P56440; O02778;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).  
GN CCR5 OR CMKBR5.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97268687; PubMed=9108095;  
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,  
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
RT "Differential utilization of CCR5 by macrophage and T cell tropic  
RT simian immunodeficiency virus strains."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;



RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97426118; PubMed=9282822;  
 RA Zacharova V., Zachar V., Goustin A.S.;  
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural  
 RT HIV type 1 host.";  
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98090115; PubMed=9430250;  
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;  
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";  
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; AF005663; AAB62557.1; -.  
 DR EMBL; U94329; AAB58446.1; -.  
 DR EMBL; AF011542; AAB65742.1; -.  
 DR EMBL; U97666; AAC51670.1; -.  
 DR EMBL; AF011540; AAB65740.1; -.  
 DR EMBL; U89797; AAC03717.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).

FT	DOMAIN	167	198	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	199	218	5 (POTENTIAL).
FT	DOMAIN	219	235	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	236	260	6 (POTENTIAL).
FT	DOMAIN	261	277	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	278	301	7 (POTENTIAL).
FT	DOMAIN	302	352	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	101	178	BY SIMILARITY.
FT	MOD_RES	3	3	SULFATION (BY SIMILARITY).
FT	MOD_RES	10	10	SULFATION (BY SIMILARITY).
FT	MOD_RES	14	14	SULFATION (BY SIMILARITY).
FT	MOD_RES	15	15	SULFATION (BY SIMILARITY).
FT	CARBOHYD	268	268	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	123	123	T -> S (IN REF. 1).
SO	SEQUENCE	352 AA;	40539 MW;	4A33E698B80FE34C CRC64;

Qy	24	FDYDY--GAPCHKKFDVKQIGAQLLPLLYSLVFI FGFVGNMLVVLILINCKKLKCLTDIYL	81
Db	10	YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFI FGFVGNMLVILILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFI ILLTIDRYLA	141
Db	70	LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIFGFFSGIFFI ILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFTGVVTSVITWLVAVFASVPGI IFTKCQKEDSVYVCGPYFP---RG	197
Db	130	IVHAVFALKARTVTFTGVVTSVITWVAVFASLPGI IFTRSQKEGLHYTCSSHPYSQYQF	189
Qy	198	WNNFHTIMRNLGLVLPLLMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	190	WKNFQTLKIVILGLVLPLLMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPI IYAFVGEKFRRYLS	317
Db	250	PYNIVLLLNTFQEFFGLNNCSSNRLDQAMQVTETLGMTHCCINPI IYAFVGEKFRNYLL	309
Qy	318	VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
Db	310	VFFOKHIAKRFCCKCSI FOOEAPERASSVYTRSTGEOEISVGL	352

OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 72.1%; Score 1370; DB 1; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 3.5e-76;  
 Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

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Db      10 YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69

QY      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      ||||| ||| :|:| ||| || :| ||| ||:| |||| ||:| ||||| ||||| |||
Db      70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129

QY      142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197
      ||||| ||||| ||||| ||||| :||| ||| :||| ||| :||| :
Db      130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHPYSQYQF 189

QY      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
      | || |: ||||| :||| ||||| ||||| ||||| :||| ||||| |||
Db      190 WKNFQTLKIVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249

QY      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      ||||: ||||| ||||| :|| |::||| ||||| ||||| ||||| ||||| |||
Db      250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

QY      318 VFFRKHITKRFCQKCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      |||: ||| ||||| | :| :| : | ||||| : ||
Db      310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352

```

# RESULT 12

CKR5\_GORGO

```

ID   CKR5_GORGO          STANDARD;          PRT;   352 AA.
AC   P56439;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97268687; PubMed=9108095;
RA   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA   Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA   Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT   "Differential utilization of CCR5 by macrophage and T cell tropic
RT   simian immunodeficiency virus strains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC   MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC   INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC   IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC   DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -----
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 CC -----

DR EMBL; AF005659; AAB62553.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 72.0%; Score 1368; DB 1; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 4.7e-76;  
 Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
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 Db 10 YDIDYYTSEPCQKTNVQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69  
 Qy 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
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 Db 70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129  
 Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197  
 |||||:|||||:|||||:|||||: ||| | | :|| :  
 Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189  
 Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIIFTIMIVYFLFWT 257  
 | || |: |||||:|||||:|||||:|||||:|||||:|||||  
 Db 190 WKNFQTLKIVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 249  
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
 ||||:|||||:|| |::||| |||||:|||||:|||||:|||||  
 Db 250 PYNIVLLLNTFQEFFGLNCSNNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy 318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360  
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 Db 310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352

RESULT 13

CKR5\_PAPHA

ID CKR5\_PAPHA STANDARD; PRT; 352 AA.  
 AC P56441;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Papio hamadryas (Hamadryas baboon), and  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9557, 9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.hamadryas;  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.hamadryas;  
 RX MEDLINE=99210133; PubMed=10195758;  
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;  
 RT "Species-specific changes in the CCR5 gene from African and Asian  
 RT nonhuman primates."  
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.anubis;  
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL; AF005658; AAB62552.1; -.  
DR EMBL; AF105287; AAD20556.1; -.  
DR EMBL; AF105288; AAD20557.1; -.  
DR EMBL; AF105289; AAD20558.1; -.  
DR EMBL; AF105290; AAD20559.1; -.  
DR EMBL; AF023452; AAC63830.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 142 166 4 (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 218 5 (POTENTIAL).  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 236 260 6 (POTENTIAL).  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 101 178 BY SIMILARITY.  
FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 72.0%; Score 1368; DB 1; Length 352;  
Best Local Similarity 76.1%; Pred. No. 4.7e-76;  
Matches 261; Conservative 31; Mismatches 45; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
:| || || | :||| |:|||||:|||||:|||||:|| :|||  
Db 10 YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69  
  
Qy 82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
|||||||:|:| ||| || :| ||| ||:| ||| ||:| |||||  
Db 70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNMTCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129  
  
Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197  
|||||||:|||||:|||||:|:| ||| || :|| :  
Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHPYSQYQF 189  
  
Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257  
||| |: |||||:|||||:|||||:|||||:|||||  
Db 190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249





RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98049523; PubMed=9388201;  
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;  
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts  
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for  
 RT polymorphisms within the regulatory regions and noncoding exons.";  
 RL J. Biol. Chem. 272:30662-30671(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.  
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,  
 RA Debre P.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [9]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=96260017; PubMed=8649511;  
 RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,  
 RA di Marzio P., Marmor S., Sutton R.E., Hill C.M., Davis C.B.,  
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;  
 RT "Identification of a major co-receptor for primary isolates of  
 RT HIV-1.";  
 RL Nature 381:661-666(1996).  
 RN [10]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=96260018; PubMed=8649512;  
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,  
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,  
 RA Paxton W.A.;  
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor  
 RT CC-CKR-5.";  
 RL Nature 381:667-673(1996).  
 RN [11]  
 RP SULFATION.  
 RX MEDLINE=99189752; PubMed=10089882;  
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,  
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;  
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
 RT entry.";  
 RL Cell 96:667-676(1999).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

```

CC      INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC      IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC      DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC      SYNCYTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC      VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC      -!- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
CC      -!- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
CC      GLYCOSYLATION.
CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```

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DR EMBL; X91492; CAA62796.1; -.  
DR EMBL; U54994; AAC50598.1; -.  
DR EMBL; U57840; AAB17071.1; -.  
DR EMBL; U95626; AAB57793.1; -.  
DR EMBL; U83326; AAC51797.1; -.  
DR EMBL; AF011500; AAB65700.1; -.  
DR EMBL; AF011501; AAB65701.1; -.  
DR EMBL; AF011502; AAB65702.1; -.  
DR EMBL; AF011503; AAB65703.1; -.  
DR EMBL; AF011505; AAB65705.1; -.  
DR EMBL; AF011506; AAB65706.1; -.  
DR EMBL; AF011507; AAB65707.1; -.  
DR EMBL; AF011508; AAB65708.1; -.  
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DR EMBL; AF011510; AAB65710.1; -.  
DR EMBL; AF011511; AAB65711.1; -.  
DR EMBL; AF011512; AAB65712.1; -.  
DR EMBL; AF011513; AAB65713.1; -.  
DR EMBL; AF011514; AAB65714.1; -.  
DR EMBL; AF011515; AAB65715.1; -.  
DR EMBL; AF011516; AAB65716.1; -.  
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DR EMBL; AF011525; AAB65725.1; -.  
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DR EMBL; AF011529; AAB65729.1; -.  
DR EMBL; AF011530; AAB65730.1; -.  
DR EMBL; AF011531; AAB65731.1; -.  
DR EMBL; AF011532; AAB65732.1; -.



Qy	198	WNNFHTIMRNI LGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
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Db	190	WKNFQTLKIVILGLVLP LLVMVICYSGILKTL LRCRNEKKRHRAVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS	317
		:               :       : :	
Db	250	PYNIVLLLNTFQEFFGLNNCSSNRDLQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL	309
Qy	318	VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAGL	360
		:                 :   :   : :             :	
Db	310	VFFQKHIAKRFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL	352

RESULT 15

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CKR5_TRAPH
ID   CKR5_TRAPH          STANDARD;          PRT;   352 AA.
AC   O97879;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN   CCR5 OR CMKBR5.
OS   Trachypithecus phayrei (Phayre's leaf monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Trachypithecus.
OX   NCBI_TaxID=61618;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416438; PubMed=10486970;
RA   Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT   "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL   Mol. Biol. Evol. 16:1145-1154(1999).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC   MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC   INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC   IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC   DIFFERENTIATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -----
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CC   -----
DR   EMBL; AF075443; AAD19855.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

```

FT	DOMAIN	1	30	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	31	58	1 (POTENTIAL).
FT	DOMAIN	59	68	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	69	89	2 (POTENTIAL).
FT	DOMAIN	90	102	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	103	124	3 (POTENTIAL).
FT	DOMAIN	125	141	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	142	166	4 (POTENTIAL).
FT	DOMAIN	167	198	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	199	218	5 (POTENTIAL).
FT	DOMAIN	219	235	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	236	260	6 (POTENTIAL).
FT	DOMAIN	261	277	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	278	301	7 (POTENTIAL).
FT	DOMAIN	302	352	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	101	178	BY SIMILARITY.
FT	MOD_RES	3	3	SULFATION (BY SIMILARITY).
FT	MOD_RES	10	10	SULFATION (BY SIMILARITY).
FT	MOD_RES	14	14	SULFATION (BY SIMILARITY).
FT	MOD_RES	15	15	SULFATION (BY SIMILARITY).
SQ	SEQUENCE	352 AA;	40509 MW;	4366F148D3A5938F CRC64;

Query Match 71.7%; Score 1363; DB 1; Length 352;  
 Best Local Similarity 75.8%; Pred. No. 9.4e-76;  
 Matches 260; Conservative 31; Mismatches 46; Indels 6; Gaps 2;

Qy	24	FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
		:          :      :      :      :   :	
Db	10	YDIDYTTSEPCQKVNKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA	141
		: :       :        :       :	
Db	70	LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG	197
		:      :      : :      :   :	
Db	130	IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHPYSQYQF	189
Qy	198	WNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	257
		:       :      :      :	
Db	190	WKNFQTLKIVILGLVLPPLVMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS	317
		:      :    ::	
Db	250	PYNIVLLNTFQEFFGLNCSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL	309
Qy	318	VFFRKHITKRCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
		:          :  :  :         :	
Db	310	VFFQKHIKRCKCCSIFQQEAPERASSVYTRSTGEQEISVGL	352

Search completed: November 25, 2003, 23:19:39  
 Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 23:15:34 ; Search time 41 Seconds  
(without alignments)  
2265.828 Million cell updates/sec

Title: US-09-625-573-4  
Perfect score: 1900  
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVTSNTNPSTGEQEVSAAGL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description
-----						

1	1392	73.3	352	6	Q95NC2	Q95nc2 callicebus
2	1375	72.4	352	6	O77776	O77776 cercocebus
3	1375	72.4	352	6	Q9MZA0	Q9mza0 callithrix
4	1375	72.4	352	6	Q8HZT9	Q8hzt9 saimiri sci
5	1373	72.3	352	6	Q95NE1	Q95ne1 cercocebus
6	1371	72.2	352	6	Q95NC4	Q95nc4 ateles geof
7	1371	72.2	352	6	Q9XT12	Q9xtl2 cercopithec
8	1371	72.2	352	6	Q95NC9	Q95nc9 alouatta se
9	1368	72.0	352	6	Q9TV49	Q9tv49 cercocebus
10	1368	72.0	352	6	O18770	O18770 pan troglod
11	1367	71.9	352	6	Q9MZ99	Q9mz99 ateles sp.
12	1366	71.9	352	6	Q95NC0	Q95nc0 hylobates m
13	1366	71.9	352	6	Q95ND1	Q95nd1 mandrillus
14	1365	71.8	352	6	Q95NC5	Q95nc5 hylobates s
15	1365	71.8	352	6	Q9XS99	Q9xs99 gorilla gor
16	1364	71.8	352	6	Q95NC1	Q95nc1 theropithec
17	1364	71.8	352	6	O97975	O97975 macaca arct
18	1364	71.8	352	6	Q95ND2	Q95nd2 mandrillus
19	1364	71.8	352	6	Q95ND0	Q95nd0 erythrocebu
20	1363	71.7	352	6	Q9TV93	Q9tv93 macaca arct
21	1363	71.7	352	6	Q9TV50	Q9tv50 pan troglod
22	1362	71.7	352	6	Q95NC8	Q95nc8 colobus pol
23	1361	71.6	352	6	Q95NC7	Q95nc7 nasalis lar
24	1361	71.6	352	6	Q9XT13	Q9xtl3 papio anubi
25	1360	71.6	352	6	Q9TSK1	Q9tsk1 cercopithec
26	1360	71.6	352	6	Q9XS35	Q9xs35 macaca neme
27	1360	71.6	352	6	Q9TV42	Q9tv42 cercopithec
28	1360	71.6	352	6	O97962	O97962 pygathrix a
29	1359	71.5	352	6	Q9TV48	Q9tv48 cercopithec
30	1358	71.5	352	6	Q9XT14	Q9xtl4 colobus gue
31	1358	71.5	352	6	Q95NC3	Q95nc3 miopithecus
32	1358	71.5	352	6	O18771	O18771 pan troglod
33	1358	71.5	352	6	O18772	O18772 pan troglod
34	1357	71.4	339	6	Q9TUV8	Q9tuv8 saguinus sp
35	1357	71.4	352	6	Q9XT76	Q9xt76 cercopithec
36	1357	71.4	352	6	Q9TV46	Q9tv46 cercopithec
37	1357	71.4	352	6	Q95NE8	Q95ne8 cercopithec
38	1356	71.4	352	6	Q9TV44	Q9tv44 cercopithec
39	1355	71.3	352	6	Q9BGN5	Q9bgn5 cercopithec
40	1354	71.3	352	6	Q9MZA3	Q9mza3 hylobates a
41	1353	71.2	339	6	Q9TSN3	Q9tsn3 macaca fasc
42	1353	71.2	339	6	Q9TQT3	Q9tqt3 callithrix
43	1353	71.2	352	6	Q95NC6	Q95nc6 trachypithe
44	1352	71.2	352	6	Q9TV47	Q9tv47 cercopithec
45	1351	71.1	339	6	Q9TUV2	Q9tuv2 alouatta ca

#### ALIGNMENTS

##### RESULT 1

Q95NC2

ID Q95NC2 PRELIMINARY; PRT; 352 AA.

AC Q95NC2;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE C-C chemokine receptor 5.  
GN CCR5.  
OS Callicebus moloch (Dusky titi).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;  
OC Callicebus.  
OX NCBI\_TaxID=9523;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
RT phylogeny.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF177887; AAK43370.1; -.  
DR InterPro; IPR000923; BlueCu\_1.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PROSITE; PS00196; COPPER\_BLUE; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 73.3%; Score 1392; DB 6; Length 352;  
Best Local Similarity 75.4%; Pred. No. 4.6e-113;  
Matches 263; Conservative 30; Mismatches 50; Indels 6; Gaps 2;

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Qy      18 EEVTTFFDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIQFVGNMLVVLILINCKKLKC 75
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 EVSSPIYDIDYGASEPCQKIDVKQMGAGLLPPLYSMVFLQFVGNMLVVLILINCKRLKS 63

Qy      76 LTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIIFFIILLT 135
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 MTDIYLLNLAISDLFFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIFGFFSGIIFFIILLT 123

Qy     136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     124 IDRYLAIVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFP 183

Qy     196 RG---WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIIFTIMIV 251
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     184 FGQYRFWK NLET LKMVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIV 243

Qy     252 YFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     244 YFLFWAPYNIVLLLNTYQEFFGLNNCSSNRLDQAMQVTETLGMTHCCVNP IYAFVGEK 303

Qy     312 FRRYLSVFFRKHITKRFCQKCPVFYRETVDGVTSTNTPSTGGEQVSAGL 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     304 FRNYLLVFFQKHIKRFCCKCSIFQKEAPERANSVYTRSTGGEQEISVGL 352

```

RESULT 2  
O77776  
ID O77776 PRELIMINARY; PRT; 352 AA.  
AC O77776;



DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Chemokine receptor CCR5.  
 GN CCR5.  
 OS Cercopithecus torquatus torquatus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=81944;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1208;  
 RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,  
 RA Aguilar R., Ho D.D., Marx P.A.;  
 RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey  
 RT with a R2b-tropic simian immunodeficiency virus.";  
 RL J. Exp. Med. 0:0-0(1998).  
 DR EMBL; AF084004; AAC62472.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473D1D3 CRC64;

Query Match 72.4%; Score 1375; DB 6; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 1.4e-111;  
 Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

Qy	24	FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
		:       :     :     :     :     :     :	
Db	10	YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFVFGFVGNILVVLILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA	141
		: :         :        :         :	
Db	70	LNLAISDLLFLLTVPFWAHYAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG	197
		:     :     :  :       :    :	
Db	130	IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSPHFPYSQYQF	189
Qy	198	WNNFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
		:      :     :     :     :     :	
Db	190	WKNFQTLKIVILGLVLPPLVMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS	317
		:     :     :           :     :	
Db	250	PYNIVLLLNTFQEFFGLNCCSSNRDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL	309
Qy	318	VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
		:           :  :  :         :	
Db	310	VFFQKHIAKRCKCCSIFQQEASERASSVYTRSTGEQEISVGL	352

RESULT 3

Q9MZA0

ID Q9MZA0 PRELIMINARY; PRT; 352 AA.  
AC Q9MZA0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE CC chemokine receptor 5 (Chemokine receptor CCR5).  
GN CCR5.  
OS Callithrix jacchus (Common marmoset).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
OX NCBI\_TaxID=9483;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20317091; PubMed=10747879;  
RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,  
RA Begum K., Galvis M.C., Kostecky V., Valente A.J., Murthy K.K.,  
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;  
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene  
RT and mRNA. Potential roles for haplotype and mRNA diversity,  
RT differential haplotype-specific transcriptional activity, and altered  
RT transcription factor binding to polymorphic nucleotides in the  
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";  
RL J. Biol. Chem. 275:18946-18961(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
RT phylogeny.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22174698; PubMed=12186836;  
RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;  
RT "Blockade of HIV-1 Infection of New World Monkey Cells Occurs  
RT Primarily at the Stage of Virus Entry.";  
RL J. Exp. Med. 196:431-445(2002).  
DR EMBL; AF252554; AAF87984.1; -.  
DR EMBL; AF177878; AAK43361.1; -.  
DR EMBL; AF452614; AAN14530.1; -.  
DR InterPro; IPR000923; BlueCu\_1.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PROSITE; PS00196; COPPER\_BLUE; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;

Query Match 72.4%; Score 1375; DB 6; Length 352;  
Best Local Similarity 75.2%; Pred. No. 1.4e-111;  
Matches 258; Conservative 33; Mismatches 46; Indels 6; Gaps 2;

Qy 24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
:| ||| || | ||||:| |||||:|:| ||||| |||||:| | :|||  
Db 10 YDIDYGPSEPCRKIDVKQMGAAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL 69

```

Qy      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      |||||:| | | | | :| ||| ||: ||| ||:| |||||
Db      70 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy     142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
      |||||:| | | | | :| ||| ||: ||| ||:| |||||
Db     130 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHPFQSQYQF 189

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLFWT 257
      || | |: |||||:| |||||:| |||||: ||| | | |:| | :
Db     190 WKNFETLKMVILGLVLP LLVMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLFWA 249

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      |||||:| |||||:| | |::| ||| |||||:| |||||:| |||||
Db     250 PYNIVLLLNTYQEFFGLNNCSSNRDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLA 309

Qy     318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      |||:| || | |: | :| : | | |||||:| ||
Db     310 VFFQKHIACFCECCSIFQKEAPERANSVYTRSTGEQEISVGL 352

```

#### RESULT 4

##### Q8H9T9

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ID   Q8H9T9      PRELIMINARY;          PRT;    352 AA.
AC   Q8H9T9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Chemokine receptor CCR5.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22174698; PubMed=12186836;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 Infection of New World Monkey Cells Occurs
RT   Primarily at the Stage of Virus Entry.";
RL   J. Exp. Med. 196:431-445(2002).
DR   EMBL; AF452615; AAN14531.1; -.
KW   Receptor.
SQ   SEQUENCE    352 AA;  40542 MW;  9FC896FB7F074647 CRC64;

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Query Match          72.4%;  Score 1375;  DB 6;  Length 352;
Best Local Similarity 75.2%;  Pred. No. 1.4e-111;
Matches 258;  Conservative 32;  Mismatches 47;  Indels 6;  Gaps 2;

```

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Qy      24 FDYDYG--APCHKFDVKQIGAQLLPPLYSVLVIFGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| |||  | | | ||||:|||||:|||||:| | | | | :| | | | |
Db      10 YDIDYGPSEPCRKIDVKQMGAGQLLPPLYSVLVIFGFVGNMLVVLILINCKRLKSMTDIYL 69

Qy      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      |||||:| | | | | :| ||| ||: ||| ||:| |||||
Db      70 LNLAISDLLFLFTIPFWAHYAAGQWDFGNTMCQFLTALYFIGFFSGIFFIILLTIDRYLA 129

```

Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197  
 |||||:|||||:|||||: ||| | | :|| |  
 Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYSCSPHFPFSQYRF 189  
 Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257  
 | | | : |||||:|||||:|||||:|||||:|||||  
 Db 190 WKNFETLKMVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 249  
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
 |||||:|:|: | |||:| | :|:| ||| |||||:|||||: |||  
 Db 250 PYNIVLLINTYPDFGFGVNNCNSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLV 309  
 Qy 318 VFFRKHITKRFCQKCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360  
 :||:| ||| | : | : | : | | ||||:| ||  
 Db 310 IFFQKHIAKRFCCKCSIFQKEAPERANSVYTRSTGEQEISVGL 352

# RESULT 5

Q95NE1

ID Q95NE1 PRELIMINARY; PRT; 352 AA.  
 AC Q95NE1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Chemokine receptor CCR5.  
 GN CCR5.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Palacios E., Digilio L., McClure H.M., Chen Z., Marx P.A.,  
 RA Goldsmith M.A., Grant R.M.;  
 RT "Parallel evolution of CCR5-null phenotypes in humans and in a natural  
 RT host of simian immunodeficiency virus.";  
 RL Curr. Biol. 0:0-0(1998).  
 DR EMBL; AF079472; AAC31193.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 SQ SEQUENCE 352 AA; 40503 MW; EBA1E633D40E9F9E CRC64;

Query Match 72.3%; Score 1373; DB 6; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 2.1e-111;  
 Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
 :| || | | :||| | :|||||:|||||:|||||:|| :|||  
 Db 10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69  
 Qy 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
 |||||:|:| ||| || :| ||| ||:| |||| ||:| |||||:|||||  
 Db 70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIFGFFSGIFFIILLTIDRYLA 129

Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----	RG	197
		:         :         :   :       :		
Db	130	IVHAVFALKARTVTFGLVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSPHFPYSQYQF		189
Qy	198	WNNFHTIMRNI LGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVI FTIMIVYFLFWT		257
		:           :		
Db	190	WKNFQTLKIVILGLVLPLLMVICYSGILKTLLRCRNEKKRHRAVRLI FTIMIVYFLFWA		249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLG MTHCCINPI IYAFVGEKFRRYLS		317
		:           :       : :		
Db	250	PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLG MTHCCINPI IYAFVGEKFRNYLL		309
Qy	318	VFFRKHITKRFCQCPVFYRETVDGVTSTNPSTGEQEVSAGL		360
		:               :   :   :   :           :		
Db	310	VFFOKHIAKRECKCCSIFOOEASERASSVYTRSTGEQEISVGL		352

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RESULT 6
Q95NC4
ID   Q95NC4          PRELIMINARY;          PRT;    352 AA.
AC   Q95NC4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   C-C chemokine receptor 5.
GN   CCR5.
OS   Ateles geoffroyi (Black-handed spider monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
OX   NCBI_TaxID=9509;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RT   "Sequence comparison of the CCR5 gene in primates and primate
RT   phylogeny.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF177885; AAK43368.1; -.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE    352 AA;  40440 MW;  F0A686CB4FE3964B CRC64;

Query Match          72.2%;  Score 1371;  DB 6;  Length 352;
Best Local Similarity 75.2%;  Pred. No. 3.1e-111;
Matches 258;  Conservative 32;  Mismatches 47;  Indels 6;  Gaps 2;

Qy      24 FDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFI FGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| |||| || | ||||:| |||||:|:|:|||||||:|:|:| | :|||
Db      10 YDIDYGASEPCRKTDVQKMGHAHLLPPLYSMVFLFGFVGNMLVVLILVNCKRPKSMTDIYL 69

Qy      82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA 141

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      ||||| ||||| :| ||| || :| ||| ||: |||| ||:| ||||| ||||| |||||
Db      70 LNLAISDLLFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy      142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
      ||||| ||||| ||||| :| ||||| :| ||||| :| ||||| :| ||| | | | :| ||| |
Db      130 IVHAVFALKARTVTFGVMTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHPFPFGQYQF 189

Qy      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
      | | | | :| ||||| ||||| :| ||||| ||||| ||||| ||||| :| ||||| |||||
Db      190 WKNFETLKMVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 249

Qy      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      ||||| :| ||||| :| ||||| :| ||||| :| ||||| :| ||||| :| ||||| ||
Db      250 PYNIVLLLNTYQEFFGLNNCSSNRDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLL 309

Qy      318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
      |||: ||| | ||: | :| :| :| | | ||||| :| |||
Db      310 VFFQKHIACFCECCSIFQKEAPERANSVYTRSTGEQEISVGL 352

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# RESULT 7

Q9XT12

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ID   Q9XT12      PRELIMINARY;          PRT;   352 AA.
AC   Q9XT12;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CC chemokine receptor 5.
GN   CCR5.
OS   Cercopithecus neglectus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=36227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spearman P.W., Mburu D.N., Graham B.S.;
RT   "Differential Utilization of CCR5 Molecules from Three East African
RT   Simian Species by the HIV-1 Envelope Glycoprotein.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF141641; AAD32686.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   352 AA;  40525 MW;  A3D86D0D0F224ED7 CRC64;

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Query Match          72.2%;  Score 1371;  DB 6;  Length 352;
Best Local Similarity 76.4%;  Pred. No. 3.1e-111;
Matches 262;  Conservative 30;  Mismatches 45;  Indels 6;  Gaps 2;

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```

Qy      24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| ||| ||| | :||| | :||| ||||| ||||| :| ||||| ||||| :| |||||
Db      10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69

```

Qy 82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
 |||||:|:| ||| || :| ||| ||:| ||||| |:| ||||| |||||  
 Db 70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197  
 ||||| ||||| ||||| |||||: |||||: |||||: |:| | | :|| :  
 Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGFHYTCSSHPYSQYQF 189

Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257  
 | | | |: | ||||| ||||| ||||| ||||| |||||: ||||| |||||  
 Db 190 WKNFQTLKTVILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWA 249

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
 |||||: ||||| |||||: || |:: |||| | ||||| ||||| ||||| ||||| ||  
 Db 250 PYNIVLLLNTFQEFFGLNNCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy 318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360  
 |||: ||| ||||| | :| :| : :| | |||||: | ||  
 Db 310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352

# RESULT 8

Q95NC9

ID Q95NC9 PRELIMINARY; PRT; 352 AA.  
 AC Q95NC9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE C-C chemokine receptor 5.  
 GN CCR5.  
 OS Alouatta seniculus (Howler monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;  
 OC Alouatta.  
 OX NCBI\_TaxID=9503;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Ryder O.A., Zhang Y.;  
 RT "Sequence comparison of the CCR5 gene in primates and primate  
 RT phylogeny.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF177880; AAK43363.1; -.  
 DR InterPro; IPR000923; BlueCu\_1.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00196; COPPER\_BLUE; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40420 MW; 3DBB43D1CCA48687 CRC64;

Query Match 72.2%; Score 1371; DB 6; Length 352;  
 Best Local Similarity 75.2%; Pred. No. 3.1e-111;  
 Matches 258; Conservative 30; Mismatches 49; Indels 6; Gaps 2;

Qy 24 FDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81

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Db      10 YDIDYGASEPCQKTDVKQMGHLLPPLYSIVFLFGFVGNMLVVLILINCKRPKSMTDIYL 69
Qy      82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db      70 LNLAISDLFFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129
Qy      142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
Db      130 IVHAVFALKARTVTFGVVTSVTTWVAVFASLPGIIFTRSQKEGYHYTCSPHFPFGQYQF 189
Qy      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
Db      190 WKNFETLKMVILGLVLP LLVMVICYSGILKTLLRCRNEKKRHRAVRILFAIMIVYFIFWA 249
Qy      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
Db      250 PYNIVLLLNTYQEFFGLNNCSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLL 309
Qy      318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
Db      310 VFFQKHIAKRFCCKCSIFQKEAPERANSVYTRSTGEQEISVGL 352

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# RESULT 9

Q9TV49

ID Q9TV49 PRELIMINARY; PRT; 352 AA.

AC Q9TV49;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE CC chemokine receptor type 5 (C-C chemokine receptor 5).

GN CCR5.

OS Cercopithecus galeritus (Agile mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus.

OX NCBI\_TaxID=9532;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=4;

RX MEDLINE=99335215; PubMed=10408730;

RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,

RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;

RT "Mutations in CCR5-coding sequences are not associated with SIV

RT carrier status in African nonhuman primates.";

RL AIDS Res. Hum. Retroviruses 15:931-939(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=4;

RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,

RA Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Zhang Y., Ryder O.A., Zhang Y.;

RT "Sequence comparison of the CCR5 gene in primates and primate



RT phylogeny.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF035215; AAD44008.1; -.  
 DR EMBL; AF177898; AAK43381.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40479 MW; 5E1504A9B87278B2 CRC64;

Query Match 72.0%; Score 1368; DB 6; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 5.6e-111;  
 Matches 261; Conservative 31; Mismatches 45; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
 :| || | | :||| |:||||| ||||| :||| ||||| :||| :||| |  
 Db 10 YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69  
 Qy 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
 ||||| ||||| :||| ||| | :| ||| ||| :| ||||| ||||| |||||  
 Db 70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129  
 Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197  
 ||||| ||||| ||||| ||||| :||| ||||| :||| :| | :|| :  
 Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHFPYSQYQF 189  
 Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHRVRIFTIMIVYFLFWT 257  
 | || | : ||||| ||||| :||| ||||| ||||| ||||| :||| ||||| |||||  
 Db 190 WKNFQTLKIVILGLVLP LLVMVICYSGILKTLRCRNEKKRHRVRLIFTIMIVYFLFWA 249  
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
 ||||| :||| ||||| ||||| :||| ||| :||| ||||| ||||| ||||| ||||| |||||  
 Db 250 PYNIVLLLNTFQEFFGLNNCSSNRDLQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309  
 Qy 318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQVSAGL 360  
 ||| :||| ||||| | :| :| :| | ||||| :| ||  
 Db 310 VFFQKHIKRFCCKCSIFQQEASERASSVYTRSTGEQEISVGL 352

# RESULT 10

O18770

ID O18770 PRELIMINARY; PRT; 352 AA.  
 AC O18770;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CCR5 receptor (Fragment).  
 GN CCR5.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MaCCR5-140a;

RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism";  
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).  
 DR EMBL; AF011538; AAB65738.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 352 352  
 SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;

Query Match 72.0%; Score 1368; DB 6; Length 352;  
 Best Local Similarity 76.1%; Pred. No. 5.6e-111;  
 Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
 :| || | :||| |:|||||:|||||:|||||:| :|||  
 Db 10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSMTDIYL 69  
 Qy 82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
 |||||:|:| || | :| || | |:| ||| |:| |||||  
 Db 70 LNLAISDLLFLLTVFPAHAAAQWDFGNMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129  
 Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197  
 |||||:|||||:|||||:|||||:|:| | | :| :  
 Db 130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHPYYSQYQF 189  
 Qy 198 WNNFHTIMRNILGLVLPPLLIMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVYFLFWT 257  
 | || |: |||||:|||||:|||||:|||||:|:| |||  
 Db 190 WKNFQTLKMLVILGLVLPPLVMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVYFLFWA 249  
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
 |||||:|||||:| | :| ||| |||||:|||||:| |  
 Db 250 PYNIVLLLNTFQEFFGLNNCSSCNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309  
 Qy 318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360  
 |||:| |||| | :| :| :| | ||||:| ||  
 Db 310 VFFQKHIKRFCCKCSIFQOEAPERASSVYTRSTGQEISVGL 352

# RESULT 11

Q9MZ99

ID Q9MZ99 PRELIMINARY; PRT; 352 AA.  
 AC Q9MZ99;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CC chemokine receptor 5.  
 GN CCR5.  
 OS Ateles sp. (Spider monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.  
 OX NCBI\_TaxID=9511;  
 RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20317091; PubMed=10747879;  
RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,  
RA Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K.,  
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;  
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene  
RT and mRNA. Potential roles for haplotype and mRNA diversity,  
RT differential haplotype-specific transcriptional activity, and altered  
RT transcription factor binding to polymorphic nucleotides in the  
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";  
RL J. Biol. Chem. 275:18946-18961(2000).  
DR EMBL; AF252555; AAF87985.1; -.  
DR InterPro; IPR000923; BlueCu\_1.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PROSITE; PS00196; COPPER\_BLUE; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40471 MW; 01E397C2A87DE64D CRC64;

Query Match 71.9%; Score 1367; DB 6; Length 352;  
Best Local Similarity 74.9%; Pred. No. 6.9e-111;  
Matches 257; Conservative 32; Mismatches 48; Indels 6; Gaps 2;

Qy 24 FDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81  
:| |||| | | | ||||:| |||||:|:|:| ||||| |||||:|:|:| | :|||  
Db 10 YDIDYGASEPCRKTDVKQMGHAHLLPPLYSMVFLFGFVGNMLVVLILVNCKRPKSMTDIYL 69  
Qy 82 LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
||| ||||| | :| || | | :| || | | :| |||| | :| ||||| ||||| |||||  
Db 70 LNLTISDLLFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129  
Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197  
||||||| ||||| |||||:| |||||:| |||||:| |||||:| ||| | | | :||| |  
Db 130 IVHAVFALKARTVTFGVMTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFPFGQYQF 189  
Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT 257  
| | | | : | ||||| |||||:| ||||| ||||| ||||| ||||| ||||| |||||  
Db 190 WKNFETLKMVILGLVLP LLVMVICYSGILKTL LRCRNEKKRHRAVRIFTIMIVYFLFWA 249  
Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317  
|||||:| |||:| |||||:| | :|:| ||| ||||| ||||| ||||| ||||| |||  
Db 250 PYNIVLLLNTYQEFFGLNNCSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLL 309  
Qy 318 VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360  
|||:| || | | :| | :| :| :| | | |||||:| ||  
Db 310 VFFQKHI AKCFCECCSIFQKEAPERANSVYTRSTGEQEISVGL 352

# RESULT 12

Q95NC0

ID Q95NC0 PRELIMINARY; PRT; 352 AA.  
AC Q95NC0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE C-C chemokine receptor 5.  
 GN CCR5.  
 OS Hylobates moloch (silvery gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=81572;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Ryder O.A., Zhang Y.;  
 RT "Sequence comparison of the CCR5 gene in primates and primate  
 RT phylogeny."  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF177899; AAK43382.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 71.9%; Score 1366; DB 6; Length 352;  
 Best Local Similarity 75.8%; Pred. No. 8.4e-111;  
 Matches 260; Conservative 30; Mismatches 47; Indels 6; Gaps 2;

Qy	24	FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
		:         :         :         :         :         :	
Db	10	YDIDYYTSGPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA	141
		:  :          :          :          :	
Db	70	LNLAISDLFFLLTVPFWAHYAAQWDFGNMTCQLLTGLYFIGFFSGIIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG	197
		:          :          :	
Db	130	IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHPYFSQYQF	189
Qy	198	WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT	257
		:          :          :          :	
Db	190	WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS	317
		:          :          :          :	
Db	250	PYNIVLLLNTFQEFFGLNNCSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL	309
Qy	318	VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
		:              :  :  :  :  :          :	
Db	310	VFFQKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL	352

# RESULT 13

Q95ND1

ID Q95ND1 PRELIMINARY; PRT; 352 AA.  
 AC Q95ND1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.  
OS Mandrillus sphinx (Mandrill) (Papio sphinx).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Mandrillus.  
OX NCBI\_TaxID=9561;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
RT phylogeny.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF177877; AAK43360.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40510 MW; 402D8543DDD3AEDD CRC64;

Query Match 71.9%; Score 1366; DB 6; Length 352;  
Best Local Similarity 76.1%; Pred. No. 8.4e-111;  
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

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Qy      24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFI PGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| ||      || | :||| | ||||| ||||| :||| ||||| :|||
Db      10 YDIDYYTSEPCQKINVQIAAHLPLPLYSLVFI PGFVGNILVVLILINCKRLKSMTDIYL 69

Qy      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA 141
      ||||| ||||| :| :| ||| || :| ||| || :| ||||| |||||
Db      70 LNLAISDLLFLLTVPFWAHYAAAQWDFGNIMCQLLTGLYFIGFFSGIIFFIILLTIDRYLA 129

Qy     142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---RG 197
      ||||| ||||| ||||| ||||| :||| ||||| :| :| ||| :|
Db     130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHPYYSQYQF 189

Qy     198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
      | || | : ||||| ||||| :||| ||||| ||||| ||||| |||||
Db     190 WKNFRTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWA 249

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS 317
      ||||| :||| ||||| ||||| :| ||| ||||| ||||| ||||| |||||
Db     250 PYNIVLLLNTFQEFFGLNNCSSNRDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy     318 VFFRKHITKRFCCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360
      ||| :||| ||||| | :| :| :| ||||| :| ||
Db     310 VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGQEISVGL 352

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RESULT 14  
Q95NC5  
ID Q95NC5 PRELIMINARY; PRT; 352 AA.  
AC Q95NC5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)



DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CC chemokine receptor 5.  
 GN CCR5.  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX NCBI\_TaxID=9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GorillaCCR;  
 RX MEDLINE=99210133; PubMed=10195758;  
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;  
 RT "Species-specific changes in the CCR5 gene from African and Asian  
 RT nonhuman primates.";  
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
 DR EMBL; AF105291; AAD20560.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 71.8%; Score 1365; DB 6; Length 352;  
 Best Local Similarity 75.8%; Pred. No. 1e-110;  
 Matches 260; Conservative 31; Mismatches 46; Indels 6; Gaps 2;

Qy	24	FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFI	FGFVGNMLVVLILINCKKLKCLTDIYL	81
Db	10	YDIDYYTSEPCQKTNVKQIAARLLPPLYSLVFI	FGFVGNMLVILILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGG	IFFIILLTIDRYLA	141
Db	70	LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSG	IFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP	---RG	197
Db	130	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKQKEGLHYTCSSHPYSQYQF		189
Qy	198	WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT		257
Db	190	WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWA		249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS		317
Db	250	PYNIVLLLNTFQEFFGLNNCSSNRDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL		309
Qy	318	VFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSA	GL	360
Db	310	VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL		352

Search completed: November 25, 2003, 23:20:33  
 Job time : 42 secs